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Minimum DB seq
Maximum DB seq
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | c | | | | | Result |
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| 202.8 | 204.4 | 204.4 | 221 | 227.8 | 299 | 366.2 | 1503.8 | 1521.2 | Score | |
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| 1614 | 1614 | 1614 | 2404 | 39796 | 554 | 657 | 1600 | 1874 | Match Length DB | |
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| AAD22071 | AAD22072 | AAD22070 | ABI99254 | AAC61681 | AAD17170 | AAQ25722 | AAC61678 | AAD33667 | ID | |
| Dermacentor variab | Dermacentor variab | Dermacentor variab | Mouse ischaemic co | Nucleotide sequenc | Human ion channel- | GABA-A receptor be | cDNA sequence enco | Human TRICH-22 cDN | Description | |

| 5 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 |
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| 156.2 | 156.4 | 156.4 | 157.2 | 157.8 | 157.8 | 158.8 | 161 | 161.2 | 162.6 | 162.6 | 162.6 | 165.4 | 165.8 | 166.2 | 166.2 | 167 | 168 | 170.2 | 171.8 | 174.2 | 179 | 181.2 | 181.2 | 181.6 | 182.2 | 182.2 | 186 | 187 | 187.6 | 187.6 | 187.6 | 187.6 | 187.6 | 189.8 | 193 |
| | 9.5 | | ٠ | | • | | • | • | - | | | - | | 10.1 | | 10.2 | • | • | • | 10.6 | • | • | • | 11.1 | 11.1 | 11.1 | 11.3 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.6 | 11.8 |
| 1408 | 1866 | 1866 | 1884 | 1844 | 1657 | 1884 | 2073 | 1297 | 1608 | 1458 | 1458 | 3619 | 2034 | 1879 | 1879 | 3598 | 1368 | 1594 | 3442 | 1640 | 3958 | 1766 | 1766 | 1609 | 2310 | 2310 | 534 | 4621 | 2400 | 2289 | 2138 | 1197 | 1197 | 1359 | 1555 |
| 14 | 15 | 14 | 20 | 20 | 19 | 20 | 22 | 20 | 22 | 23 | 22 | 23 | 22 | 22 | 22 | 22 | 20 | 24 | 22 | 24 | 17 | 22 | 22 | 24 | 15 | 14 | 21 | 24 | 22 | 22 | 22 | 24 | 22 | 24 | 17 |
| AAQ33130 | AAQ69143 | AAQ33131 | AAV83111 | AAV64372 | AAV55008 | AAV83112 | AAH78309 | AAX24373 | AA168566 | ABL12887 | AAI68567 | ABL13035 | AAH78310 | AAD04275 | AAD04274 | AAD21372 | AAX24372 | ABI99308 | AAD21373 | AAD26938 | AAT43596 | AAD04277 | AAD04276 | AAD26937 | AAQ69141 | AAQ33129 | AAC61680 . | AAD26939 | AAD21397 | AAD21396 | AAD21395 | AAD22082 | AAD21378 | ABK27334 | AAT28989 |
| GABA-A receptor al | Human GABA recepto | GABA-A receptor be | | GABA-gated chlorid | GABA gated chlorid | | Nucleotide sequenc | Cat flea glutamate | D. melanogaster li | Drosophila melanog | D. melanogaster li | | eotide seque | form of S. | Long form of S. am | Dermacentor variab | | Mouse ischaemic co | Dermacentor variab | sp. F | o o | form of s | of, | | Human GABA recepto | GABA-A receptor al | Nucleotide sequenc | Heliothis virescen | R. sanguineus glut | | sanguineus | sanguineus | R. sanguineus LGIC | gamma- | Human GABA-A recep |

ALIGNMENTS

RESULT 1 AAD33667 Human TRICH-22 cDNA 01-JUL-2002 (first entry) AAD33667 standard; cDNA; 1874 BP

Human; transporter and ion channel; TRICH-22; transport disorder; angina; amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer; depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease; cell proliferated disorder; infertility; arteriosclerosis; gene therapy; Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy; myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension; acquired immune deficiency syndrome; immunological disorder; scleroderma; endocrine disorder; autoimmune thyroidittis; rhemmatold arthritis; goltre; cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection; epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease; muscle disorder: stroke, Amenoria, anviatur. Alto: asthma. epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's dismuscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;

Homo sapiens.

sig_peptide /product= 286..369 Location/Qualifiers 286..1539 /*tag= /*tag= "Human TRICH-22 protein"

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CC Arteriosclerosis, atherosclerosis, bursitis, hepatitis and parkinson's CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's CC disease, multiple sclerosis, dementia and other extrapyramidal disorder. CC motor neuron disorder, prion disease, metabolic disease of the nervous system and other developmental disorders of the central nervous system, cc neuromuscular disorders, metabolic, endoorine and toxic myopathies, CC periodic paralysis, mental disorders including mood, anxiety; and cimmunological disorders include acquired immune deficiency syndrome CC (AIDS), adult respiratory distress syndrome, Addison's disease, CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic callergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis, CC systemic luques erythematosus, systemic sclerosis, ulcerative colitis, chaemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal, chaemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal, CC haemodialysis, uveitis, polymyositis, arrhythmias and hypertension. The CC raict polynucleotides are used in gene therapy. The present sequence is human TRICH-22 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2000;
18-AUG-2000;
25-AUG-2000;
31-AUG-2000;
08-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 96; Page 220-221; 230pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reddy R
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Query Match

Sequence

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467 G; 461 T; 0 other;

Score

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying a characterizing genetic defect involved in the disorders and disease related to ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid sequence encoding human ataxia protein for compounds useful for treating disorders relating to mutations
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                                                                                                                                                             GGTTTGGACAGTTCCTTGCTGATCTCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTA
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               CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTTGAGTGGC
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TTGGTTATACCATGAACGACCTCATCTTTGAGTG - -

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The sequence given is the gamma-aminobutyric acid (GABA) A receptor beta-subunit. This sequence is used in an expression plasmid operably linked to the tac promoter, a ribosome binding sequence, the E. coli outer membrane protein Ompr signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycine receptor alpha-subunit. This expression plasmid can be used to transform E. coli to produce an N-terminal extracellular site protein of ion channel direct binding type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                             prepn. of N-terminal extracellular site protein - l E.coli transformed by a plasmid comprising the tac binding site, etc.
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Score 366.2; DB 13;
pred. No. 1.6e-94;
0; Mismatches 133;
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RESULT 4
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AC AAD17170;
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AC AAD17170;
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Comman ion channel-93 (ion9)
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Human ion channel-93 (ion9)
XX
Human; ion channel-93; ions
XX
Human; ion channel; neuro
XX
Human; ion channel; ions
XX
Human; ion channel polynucleo
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                                                             New ion channel polynucleotides and polypeptides, useful for identification of ion channel modulators and treatment of mental disorders, infections, cancer and autoimmune diseases -
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/transl_except= (pos:138..146, aa:Asp-Ala)
/note= "This translational exception comprises
in-frame stop codon insertion; CDS does not inc
start and stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 554 BP; 158 A; 124 C; 135 G; 137 T; 0 other;
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Pred. No. 2.
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.8e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the human ataxia gene. The ataxia protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying and characterizing genetic defect involved in the disorders and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
         Mouse
                              07-MAR-2002
                                                    ABI99254
                                                                        ABI99254 standard;
                                                                                                                                                                                                                                                                                                                                                    Sequence 39796 BP; 10630 A;
                                                                                                                                                                                                                                                                                                                                                                         related
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compounds useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RAPP/) RAPPOLD-HOERBRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
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                                                                                                                                                                                                                                                                          263 CCACAATGGACTACCGGGTGAATGTCTTCCTTGCGGCAACAGTGGAATGACCCACGCCTGT
                                                                                                                                                                                                                                                                                                         232;
         ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Page 22-44; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                         to ataxia
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                               CCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTTCCATGCTGGACTCTATCT
                                                                                                                                        ACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACC 501
                                                                                                                                                                                   GGAAGCCAGACCTCCTTCGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGG
                                                                                                                                                                                                                  CCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCT
                                                                                                                                                                                                                                                              CCTCCCAGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGT
                                                                                                                             ACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGTGCACC 33983
                                                                                                                                                                        GGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGG
                                                                                                                                                                                                                                                                                                          Conservative
                             (first entry)
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/*tag= h
34115..34195
         condition
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35760.
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38782..38996
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                                                                        cDNA;
                                                                                                                                                                                                                                                                                                                    13.9%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating
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                                                                         2404
         related
                                                                                                                                                                                                                                                                                                                                                    9337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding human ataxia protein for ng disorders relating to mutations
                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                        Score 227.8; DB 2
Pred. No. 7.7e-54;
0; Mismatches 7
                                                                         ВP
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         cDNA sequence
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         SEQ ID
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                                                                                                                                                                                                                                                                                                                              Length
         NO:85
                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                              39796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening in ataxia
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. AB19913 and AB19914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. expression levels of particular genes by determining the expression profile genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 265-268; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   503;
                   CAAATGAAAAAAGTGCCAATTTTCATGATGTGACCCAAGAAATATCCTGTTGTTTATCT
                                                                                 CTAATGAGAAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCT
                                                                                                                                                   ACTCTCTGGACCTCGATCCCTCCATGCTGGACCTCTATCTGGAAGCCAGACCTCTTCTTTG
                                                                                                                                                                                               TCTTGAGACAGAATGGAATGACCCCAGACTCAAGCTACCTAGTGACTTCAGAGGCTCAG
                                                                                                                                                                                                                        TCTTGCGGCAACAGTGGAATGACCCACGCCT-GTCCTACCGAGAATATCCTGA-----TG
                                                                                                                                                                                                                                                               TTTTTATTAATAGTTTTGGATCCATTCAAGAGACAACAATGGACTATAGAGTTAACATTT
                                                                                                                                                                                                                                                                                                TCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCT
                                                                                                                                                                                                                                                                                                                                   GTTATGATCCCAGGATCAGACCAAACTTCAAAGGCATTCCTGTTGATGTAGTAGTCAACA
                                                                                                                                                                                                                                                                                                                                                 GATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCGTGAACGTGACCTGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2404 BP;
                                                                                                                                 ATGCACTGACAGTTGACCCCACCATGTATAAGTGCTTGTGGAAAACCTGACTTATTCTTTG
 TTCGGGATGGAGACGTCCTTGTGAGCATGAGGTTGTCTATTACACTTTCATGTCCTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a method for examining comprising measuring the expression levels
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001WO-JP04192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   705 A; 493 C; 502 G; 704 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 221; DB 24;
Pred. No. 1.5e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagata
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    occlusive ischemia) by measuring
defined in the specification or
of a gene group comprising these

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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2404;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemic
of particular
                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
 638
                                523
                                                               578
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ACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCA

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RESULT 7
AAD22070
ID AAD22070
AC AAD2
XX AAD2
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XX Gamm
KW GABA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic;
GABA-gated chloride channel; recombinant expression; domestic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dermacentor variabilis
         New polypeptide useful humans, dogs, cattle, h
                                                                                                                                                                                                                                              31-MAR-2000; 2000US-193791P
                                                                                                                                                                                                                                                                                             28-MAR-2001; 2001WO-US09955
                                                                                                                                                                                                                                                                                                                                                                                         WO200174884-A1
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                                                                                                                                                                                                (MERI ) MERCK & CO
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DB; AAE13312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 TGTTTGAGTGGCTGGAAGATGCTCCTGCTGCCAAGTGGCTGAGGGGGCTGACTCTGCCCC
ypeptide useful for preventing or treating dogs, cattle, horses, deer, or other wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGATGCTAGTGCTGCCAGAGTACCTCTGGGCATCTTCTCCGTGCTCAGTTTGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTCATTGCCTGCTGCTCTTCGGGTTTGCCTCCCTCGTGGAGTACGCTG 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTACACTTGTGGAGGTCATCTTCACCCTGAGGAGACAGGTTGGGTTCTACATGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTC
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                           ATCTGGATGGCTGTGTGTCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATA 1059
                                                                             ACCCAGAGCTCTGGCTCCGGGCCTCTTTGCCTAAGGTGTCCCTACGTGAAGGCAATCGAC
                                                                                                                         CACCGTGACGCTAGTCCAGCTCGCGTCGCGCGTCACCACCGTGCTCACGATGACC
                                                                                                                                           AACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACC
                                                                                                                                                                                      ATCCAGATCTAÇATCCCGGCCGGATTGATCGTGGTTATTTCCTGGGTCTCCTTTTGGCTC
                                                                                                                                                                                                        ATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTGGATC
                                                                                                                                                                                                                                                   GGAAACTACTCCCGCCTGGTATGTGAAATACGGTTCGCCCGCTCCATGGGCTACTACCTG
                                                                                                                                                                                                                                                                                  GGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTG
                                                                                                                                                                                                                                                                                                                   CCGCAGTTCAAGGTCCTCGGTCACGTCCAAAAAAGCC---AAAGAGGTTGCCCTAACGACA
                                                                                                                                                                                                                                                                                                                                               CCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACA
                                                                                                                                                                                                                                                                                                                                                                              ATCCGCTACCGGTGGTCGGACGGTGACACCTCCGTCCGCATCGCCAAGGAGGTAGAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCA
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GTCTACCTGGGCACATGTTTCGTAATGGTGTTTACCGCGCTCCTGGAGTACGCCGCGGTA
                                                              ACACTCATGTCCAGTACCAACGCAGCGCTGCCCAAAATATCCTACGTCAAGAGTATCGAC
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RESULT 9
AAD22071
ID AAD22071 standard; DNA; 1614 BP.

XX
AC AAD22071;
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DT 12-FEB-2002 (first entry)
XX
DE Dermacentor variabilis clone 9 GABA-gated chloride
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Best Local
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                                                                                                                                                                                                                                                                                                                                                 The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DMA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins GABA-gated chloride channel proteins. The present sequence is Dermacentor variabilis clone 9 GABA-gated manual present as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated channel proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric aci (GABA)-gated chloride channel
                                                                                                                                                                                                                                                                                                                   Sequence 1614 BP; 371 A; 474 C; 421 G; 348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zheng Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic; GABA-gated chloride channel; recombinant expression; domestic animal; ds
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                                                                     CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                                                                                                                                   GTCACTATGCAGATTATCAGCATAAGTACAGTCTCTGAAGTACAAATGGACTTTACTTCT
                                                                                                                                                                                  TGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTG
                                                                                                                                                                                                                                ACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCCACCCGTGAACGTGACC
                                                                                                                                                                                                                                                                                                                                            channel DNA
                                                                                                                    GACTTCTATTTCCGGCAATCGTGGCGGGACGAGCGACTCTCGTTCCAGAAAAGCCCCAGAC
                                                                                                                                          AATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGA-
TTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGC
                                                                                                                                                                                                                  ACACGTGGGTACGACAGGAGGGTGAGGCCAAATTATGGCGGCGTTCCAGTGGAAGTTGGC
                        TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
                                                                                            --TGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTC
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                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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                                                                                                                                                                                                                                                                               Score 202.8; DE
Pred. No. 2e-47;
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06-JAN-1997
P-PSDB; AAR97299
                 WPI; 1996-209359/21
                                                                                                                                                                                                                                                                                                                                                                                        GABA-A receptor;
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                                                                                                                                                                                                    11-APR-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human GABA-A receptor delta subunit cDNA
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                                                                                       SHARP & DOHME LTD
                                                                                                                            94GB-0020010
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                                                                                                                                                                                                                                                                                              Location/Qualifiers 47..1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding alpha-4 and delta subunit(s) of the human GABAa receptor - also stably co-transfected eukaryotic cells expressing receptors contg. these subunit(s), used for screening and designing the second control of the
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Pred. No. 1
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The invention relates to an isolated mammalian polypeptide (I), which is CC a mutant of gamma-aminobutyric acid (GABA) receptor subunit. The mutation CC disrupts the functioning of an assembled GABA receptor, its functional CC fragment or homologue, and creates a phenotype of epilepsy, anxiety, manic depression, phobic obsessive symptoms, Alzheimer's disease, CC epilepsy, anxiety, manic depression, phobic obsessive symptoms, Alzheimer's disease, CC Alzheimer's disease, schizophrenia, migraine and/or obesity. (I), the polynucleotide (II) CC useful for treating the above conditions. (I)-(III) are useful in the diagnosis of CC epilepsy, anxiety, manic depression, phobic obsessive symptoms, CC Alzheimer's disease, schizophrenia, migraine and/or obesity. (III) is CC useful for treating the above conditions. (I)-(III) are useful in CC screening of candidate pharmaceutical agents, where high-throughput CC creening techniques are employed. (II) is useful to detect and conditions of the study of the function of a GABA receptor, to study the mechanism of the disease as related to GABA receptor, for the creation of mechanism of the disease as related to GABA receptor, for the creation of
                                                                                                                                                                                                                                                                                                                                                        Mutant
useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nootropic; Neuroprotective; Neuroleptic; Antimigraine; Anorectic; gamma-aminobutyric acid receptor subunit; GABA; epilepsy; anxiety manic depression; phobic obsessive symptom; Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                       34; Page 73-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-aminobutyric acid receptor gamma-2
                                                                                                                                                                                                                                                                                                                                    gamma-aminobutyric acid receptor subunits and DNA molecule, for diagnosing epilepsy, Alzheimer's disease, migraine, obey, manic depression and schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RH,
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2001AU-0004953.
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                                              GCCATCAAGGCACTGGACGTCTACTTCTGGATCTGCTATGTCTTCGTGTTTGCCGCCCTG
                                                                          TACGTGAAGGCAATCGACATCTGGATGGCTGTGTGTCTGCTCTTTGTGTTCGCTGCCTTG 104:
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53.1%;
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Pred. No. 9.8e-44;
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CC insecticidal activity for use in treating parasitic infections in humans correctionals, as hybridisation probes to isolate related genes from other corganisms to establish additional pesticide drug screens and also used in competition. binding experiments or for functional chloride channel cassays to screen for compounds that activate, block or modulate the channel. Heterologous expression of LGIC/GluCl protein allows the pharmacological analysis of compounds active against parasitic in the treatment of tick infestations directly related to Dv. LGIC/GluCl protein acts as targets to identify modulators of the channels, where the condulators act as effective insecticidal, acaricidal, mitacidal and/or compounds active as targets to identify modulators of the channels, where the modulators act as effective insecticidal, acaricidal, mitacidal and/or compounds and human health and/or crop protection. The modulators are useful for treatment or diagnosis of specific disorders. The present sequence is Rhipicephalus sanguineus cascidal cascidal probe which is used for screening Dermacentor LGIC/GluCl 1
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                                       Matches
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a purified nucleic acid molecule encoding Dermancentor variabilis (Dv) (American dog tick) ligand gated ion channel/L-glutamate gated chloride channel (LGIC/GluCl) protein.

LGIC/GluCl DNA is useful for identifying a compound that modulates glutamate-gated channel protein activity and for identifying a modulator of LGIC/GluCl channel protein: LGIC/GluCl DNA is used for establishing novel insecticide screens, validate potential lead compounds with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel purified nucleic acid molecule encoding Dermancentor variabilis ligand gated ion channel/L-glutamate gated chloride channel protein, useful for identifying modulator compounds that are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tick; acaricide; mitacide; crop protection; nematocide; insecticide; ligand gated ion channel/L-glutamate gated chloride channel; LGIC/GluCl; parasitic infection; pesticide drug screen; tick infection; probe; ss.
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                                                                                                           Sequence 1197
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 226 AACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAAT 285
                                                        Similarity
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55.0%;
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Pred. No. 3.9e-43;
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                                GABA-gated chloride channel;
GluCl DNA; probe; ss.
                                                                                             R. sanguineus GluCl DNA probe
                                                                                                                                                                                         AAD22082 standard;
   Rhipicephalus sanguineus
                                                               Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic;
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                                                                                                                                                                                           DNA;
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                                                recombinant expression; domestic
                                                                                             to clone GABA-gated chloride channel DNA
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The invention relates to gamma aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Rhipicephalus sanguineus GluCl DNA probe which is used for cloning Dermacentor variabilis GABA-gated chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200174884-A1
                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide useful for preventing or treating tick infestation, humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric aci (GABA)-gated chloride channel -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-193791P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2001; 2001WO-US09955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO
Sequence 1197 BP; 268 A; 358 C; 311 G;
                                              channel DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cully D,
                                                                                                                                                                                                                                                                                                                                              Page 23-24; 59pp;
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                                                                                                                                                                                                                                                                                                                                                  English
          260 T; 0 other;
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acid

useful

Query Match Best Local Similarity Matches 466; Conservative 11.4%; 0; Score 187.6; DB 2 Pred. No. 3.9e-43; Mismatches DB 24; Length 1197; 334; Indels 48;

밁 Q 멍 δõ Вb οy 멍 QΥ Q g δõ 217 226 AACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAAT 285 406 157 277 646 TTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCAG 97 TCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCT 405 GTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGAC CCCAACGGCGACGTTCTCTTCAGCATCAGAATATCCTTGGTGCTTTCATGTCCGATGAAC AATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTC GTTCGCTACCTGACGCTCACCGAACCGGACAAGCTTTGGAAGCCGGACCTGTTTTTCTCC ATGACGTTCAGAGAGCAGTGGCGGGACGACGAGACTCCAGTACGACGACTTGGGCGGCCAG 216 AACATCTTTGTAAGAAGTATCGGCAGAATTGATGACGTCACCATGGAGTACACAGTGCAA 156 CTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATA AACGAGAAAGAGGGACACTTCCACAACATCATCATGCCCAACGTGCTTCTACGCATÄCAT CTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTG CTGAAATTTTATCCTTTGGATAAACAAATCTGCTCTATCGTCATGGTGAGCT---------ATGGGTATACAACAGAGGACCTGGTG 585 345 465 525 336 705 645 448 396 276 474

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                               Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                              Warmke JW,
                                                                                                                                                                                                            31-MAR-2000;
                                                                                                                                                                                                                                          28-MAR-2001;
                                                                                                                                                                                                                                                                          11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhipicephalus sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brown dog tick; glutamate-gated chloride channel; GluCl2; crop protection; insecticide; nematocide; clone Tl2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R. sanguineus glutamate-gated chloride channel 1 cDNA clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-2002
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                   acaricides
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                                                                                                                                              Cully DF
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                                                                                                                                                                                                                                                                                                                                    sanguineus GluCll protein, T12" region is specifically referred in claim
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                                                                                                                                              Hamelin
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acaricide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful for establishing functional or binding assays to identify novel GluCl1 channel modulators. The present sequence is R. sanguineus
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Best Local
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                                               1156. ACCTCGATCCCGGCGCGAGTGTCGCTGGGCGTCACCACCCTGCTCACCATGGCCACGCAG
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AGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGG
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                                                               GATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAG
                                                                                                                            ATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCTCCTTCTGGATCAACATG
                                                                                                                                                                          TACAGCTGCTTGCGCGTGGACCTGGTGTTCAAGCGCGAGTTCAGCTACTACCTGATCCAG
                                                                                                                                                                                            TTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAG
                                                                                                                                                                                                                                                          TTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAA
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                                                                                                          ATCTACATCCCGTGCTGCATGCTGGTCATCGTGTCCTGGGTGTCGTTCTGGCTCGACCCC
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                                                                                                                                                                                                                                                                                                    TTTCTATG---GAAAGAGGGGGATCCTGTACAGGTCACAAAAAATCTCCACTTGCCACGT
                                                                                                                                                                                                                                                                                                                                  TTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                 -----ATGGGTATACAACAGAGGACCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAAATTTTATCCTTTGGATAAACAAATCTGCTCTATCGTCATGGTGAGCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 A; 661 C;
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Pred. No. 5.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown dog tick; glutamate-gated chloride channel; GluCl1; GluCl2; crop protection; insecticide; nematocide; acaricide; clone T82; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD21396;
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                                                                                                                                                                                                                                                                               The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-193934P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2001; 2001WO-US09905
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                                                                                                                                         and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GLC11 and GluC12 channel functional forms are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERI ) MERCK & CO INC
  Sequence
                                                                                    for establishing functional or binding assays to identify novel GluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sanguineus glutamate-gated
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/note= "This region is specifically referred
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  509 A; 727
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                                                                                                                                                                                     AGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGG
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                                     GTTTCTCG 1073
                                                                         ACCGCCGTCTGTCTGACCTTCGTATTCGGCGCGCCTCCTCGAGTTCGCCCCTGGTCAACTAC
                                                                                                             ATGGCTGTGTGTCTCCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTT
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smatches 334;
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search completed: June 30, 2003, 21:13:05
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Query Match

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AX392950 Sequence 52 AX392950 AX392950.1

1874 bp 52 from Patent WO0212340.

DNA

linear

PAT 23-MAR-2002

GI:19700997

REFERENCE

AUTHORS

Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y., Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Walia,N.K., Gandhi,A.R., Hafalia,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result O იი ŏ 1521. 1503. 1002. 695.8 659.2 656.2 654.8 654.6 654.6 650.2 664.6 664.6 664.3 235. 232. 232. 232. 232. 230. 230. 227. Score Match 1595 100269 100269 194822 Length 1374 1679 1222 2376 1628 1418 1857 1407 В 10 9 9 10 10 10 10 10 10 10 10 0 RNO310838 0 RATIGRAS AF488379 HSGLYRA2 RNO310837 RNIGRAA2 DRE404970 RNO310839 AF214575 AF094754 AF094755 HSU35G3 AF018157 BC032635 AF268376 E03608 AL671887 AX251654 DRE308517 HS1055C14 DRE308516 DRE5812 DRE404971 AY094975 **HSGLYRA1** AX037570 HSU93917 AY094974 HSU33267 RNIGRA1 RNO310836 RNNEOGLY RNO310834 RATGLYRA1 AF362764 RNO310835 ALIGNMENTS AJ310834 Rattus no D00833 Rattus norvegicu S22008 H. sapiens a AF268375 Bos tauru S73718 Glral = inhib AJ310835 Rattus no x55246 R. norvegicu AJ308316 Danio rer AJ005812 Danio rer AJ005812 Danio rer AJ005812 Danio rer AY094975 Morone am U93917 Human glyci AY094975 Morone am AJ310836 Rattus no M55250 Rat inhibit AF488379 Danio rer AF488379 Danio rer AF362764 Mus muscu AJ308317 Danio rer AL049610 Human DNA E03608 DNA encodin AL671887 Mus muscu AX251554 Sequence AX037570 Sequence 293848 Human DNA s AF018157 Homo sapi X81202 M.musculus X52009 H. sapiens a AJ310837 Rattus no X61159 R. norvegicu X57281 Rat NG1yR m AJ310834 Rattus no AF094754 Homo sapi AF094755 Homo sapi U33267 Human glyci BC032635 Homo sapi AJ404970 Danio rer AX392950 Sequence AX037565 Sequence Description AF268376 Bos tauru AJ310839 Rattus no AF214575 Mus muscu Y00276 R.norvegiuc S73717 GLRA1-inhib AF462147 Mus muscu

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Borowsky,M.L., Lo,T.P., Lu,Y., Poliky,J.L., Greene,B.D.,
Sanjanwala,M.S., Raumann,B.E., Burford,N., Ison,C.H., Lee,E.
Ding,L., Das,D., Kallick,D.A., Khan,F.A. and Seilhamer,J.J.
Patent: WO 0212340-A 52 14-FEB-2002;
Location/Qualifiers
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Rappold-Hoerbrand,G.
Gene for ataxia
Patent: WO 0058461-A 1 05-OCT-2000;
RAPPOLD HOERBRAND GUDRUN (DE)
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                                           CCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTTGAGTGGCTGGAA
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/note="cDNA"
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/db_xref="GI:11226987"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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| Qy 364 TCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTTGCTAATGAGAAAGGGGCCAAC 423 | 184 61 244 121 304 181 | Ouery Match 61.1%; Score 1002.2; DB 10; Length 1251; Best Local Similarity 87.2%; Pred. No. 8.9e-268; Matches 1128; Conservative 0; Mismatches 123; Indels 42; Gaps 1; Oy 124 ATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGGGAACATCTGGATATGATGCCAGG 183 | /protein_id="AAL69899.1" /db_xref="GI:18448711" /db_xref="GI:18448711" /translation="MSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSV /translation="MSPSDFLDKLMGRTSGYDALESIMKPDLFFANEKGANFH ETTMOYRVANFLRQGWNDERLAYERYPDDSLDLMPSMLESIMKPDLFFANEKGANFH EVTTDNKLLRIFKNGNVLYSIRLTLILSCPMDLKNFPMDIQTCTMQLESFGYTMNDLM FEWLEDAPAVQVAEGLTLPGFILRDEKDLGYCTKHYNTGKETCIEVKFHLERQMGYYL IQMYIPSLLIVILSWYSFWINMDAAPARVGLGTTTVLTMTQSGSGRASLFKVSYXKA IDIWMAVCLLFVFAALLEYAAVNFVSRQHKEFMRLRRQGRQRMEDDIIRESFTYERG YGLGHCLQAABGGPMEGSSIYSPOPPTLLKEGETMRKLYVDRAKRIDTISRAVFPFT BASE COUNT 324 a 314 c 281 g 332 t | gene 1. 1251 /gene="Glra4" /note="mmGlra4" CDS 11251 /gene="Glra4" /fote="ligand-gated ion channel" /codon_start=1 /product="qlycine receptor alpha 4 subunit" | FEATURES LIVELING FLOOR, GERMANY SOURCE 1. 1251 STATE OF THE STATE OF | Localization of different gl spinal cord Unpublished 2 (bases 1 to 1251) Groemer, TW., Becker, CM. Direct Submission Submitted (21-DEC-2001) Bioc | " H |
|--|--|---|--|---|---|---|---|
| RESULT 4 DRE404970 LOCUS DEFINITION DANIO rerio mRNA for glycine receptor alpha22 subunit (glyR alpha ACCESSION AJ404970 VERSION KEYWORDS SOURCE ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | 11111111111111111111111111111111111111 | Qy 1144 GAAAGTCGTTTCTATTTCCGTGGCTATGGCTGGCCACGCAAGACATGGA 1203 | 964 799 1024 859 1084 919 | Qy 844 CTCATCGTCATCCTGTCCTGGGTCTCTGGATCAACATGGATGCTGCCCCTGCCCGT 903 | OY 724 ANGGATCTAGGCTGTTGTACCAGACACCAGGGAAATTCACCTGCATCGAGGTA 783 | 455TIGGCTACACCATGAATGACCTCATGTTTGAGTGGCTAGAAGAT 664 GCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAG [| Qy 544 GACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCA 603 |

| Qy 359 ATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTTCTT | Oy 179 CCAGATTCGCCCCAATTTTAAAGGCCCACCGCTGAACGTGACCTGCAACATCTTCATCA 238 | Query Match 42.4%; Score 695.8; DB 5; Length 2045; Best Local Similarity 73.6%; Pred. No. 2.2e-182; Matches 949; Conservative 0; Mismatches 292; Indels 48; Gaps 3; Qy 119 AGCCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATG 178 | DFLDKLMGRTSGYDARIFPNFKGPPVNVTCNIFINSFGSITETTMDYRLNVFLRQQWN DPRLAYSEV PDASLDLDSYMKDDLFFANEKGANFHEVTTDNKLLRIFQNGNVL YSIRLTLLISCPMDLKNFPMDIQTCMQLESFGYTMNDLIFEMLSDNFVQVVADDLTLP QFVLKEEKDLGYCTKHYNTGKFTCLEVKFHLERQWGYYLLQWYIBSLLIVLLSWYSFW INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLIVFAALLEY AAVWFVSRQHKEFIRLKKKORRQRIEEDLVRESRGFYFRGYGLGHCLQTKDGTAVEGS SVFAPPPPVQVLYDGEAVRKRFVDRAKRIDTISRAVFPLSFLIFNVFYWITTKVLRHE DIHANP" 1891. 2045 Jene="glyr alpha" 524 a 501 c 460 g 560 t | 70 | source 1. 2045 /organism="Danio rerio" /db_xref="taxon:7955" /tissue_type="brain" /dev_stage="adult" gene 1. 2045 | EFFERENCE Imboden, M AUTHORS Imboden, M Bregestov TITLE Isolation Receptor JOURNAL Unpublish EFFERENCE 2 (bases AUTHORS Goblet, C. TITLE Direct Submitted Pasteur, |
|---|--|--|---|---|--|--|
| RESULT 5 RNGRSTR ROCUS DEFINITION R.NOTVegiucus mRNA for glycine receptor strychnine binding subunit (48K). ACCESSION Y00276 VERSION Y00276 1 GI:56326 KEYWORDS SOURCE Rattus norvegicus. ORGANISM RATTUS NOTVEGICUS | Db 1730 TTTACGACGGAGAGGCCGTCCGGAAGCGTTCGTGGACCGAACGAA | Qy 1139 TCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCCTTGGGCCACTGCCTGCAGGCAA 1195 | Oy 959 GGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCTGGATGGCTGTGTC 1018 | Db 1250 AGGTGAAGTTTCACTTAGAGAGACAGATGGGCTACTATCAGATGTACATCCCCA 1309 Qy 839 GCCTACTCATCGTCATCCTGTCCTGGGTCTCCTGGATCAACATGGATGCTGCCCCTG 898 | ATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGAAATTCACCTGCATCG | Qy 539 CCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATACTCTGCAGCCCTC 598 |

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Submitted (14-JUL-1987) Gundelfinger
Submitted (name Heidelberg, FRG
                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source: strain=Wistar; tissue=spinal cord; source: clones=GR1, GR6, GR1-6, GR1-6-1; Data kindly reviewed (26-SEP-1987) by Gund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grenningloh,G., Rienitz,A., Schmitt,B., Methfessel,C., Beyreuther,K., Gundelfinger,E.D. and Betz,H.
The strychnine-binding subunit of the glycine receptor homology with nicottnic acetylcholine receptors of the strycholine receptors (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                 GAGAATATCCTGATGACTCTCTGGACCTCGATCCCTTCCATGCTGGACTCTATCTGGAAGC
                                                                                        CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA
                                                                                                                                                                                                                                       AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC
CAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACA
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GGEGRFNFSAYGMGPACLQAKGGISVAGANNNNTTNPAPAPSKSPEEMRKLFIQRAKK
DKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK"
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/product="glycine rece
/protein_id="CAA68378.
/db_xref="GI:755778"
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387 c 361 g
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/strain="Wistar"
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72.1%;
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Rodentia;
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Pred. No. 3.3e-172;
0; Mismatches 313;
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                                                                                                          TCCTCATCTTCAACATGTTCTACTGGATCATCTACAAGATCGTCCGGAGAGAGGACGTCC
                                                                                                                           TCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGTGCTATGGTCAGAAGATATCC 1402
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| Oy 356 TCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAG | 296 335 | 236 275 | Qy 176 ATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCA | 116 CCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCG. | Query Match 40.0%; Score 656.2; DB 10; Length Best Local Similarity 72.6%; Pred. No. 2.2e-171; Matches 942; Conservative 0; Mismatches 298; Indels | VSRQHKELLRFRRKRRHHKDDEGGEGRFNFSAYGMGPACLQAKDGISVKGANNNYTTN PPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK" BASE COUNT 349 a 404 c 332 g 322 t ORIGIN | YNEYPDDSLDLDPSMLDSIWK PDLFFANEKGA OUT TIED INKLLEISRUGVULS INI TLTLACPMDLKNFPMDVQTCIMOLESFOYTMNDLIFEMQEQGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTCIEARFILERQMGYYLLQMYIPSLLIVILSWIISFWINNDLYTTYDYSIXI APARVGIGITTYVITMTKTOSSGSRAGILSRUGVAVATORIAN TOTALAN AVANE | /protein_id-"aaB32157.2" /protein_id-"aaB32157.2" /db_xref-"GI:9247215 / Lassiation-"myssmilrpylwetiveeslaaskeaeaarsapkpmspsdeldk / Lightsgyddarienwysgppvmvsgniftusegstapttmnvpvmift.goownder.a | <pre>published reference; GLRAI protein; GlyR al /codon_start=1 /product="inhibitory glycine receptor alpha short form"</pre> | CDS 581407 /gene="clral" /note="alternatively spliced; This sequence comes /note="alternatively spliced; This sequence comes /note="alternatively spliced; This sequence comes | /tissue_type="brainstem and spinal cord" /note="A/HeJ" gene 1. 1407 /dene="Glrai" | cation/Qualifiers .1407 .ganism="Mus sp." cyanism="taxon:10095 | 7920629 7920629 The National Librar GenBank Staff at the National Librar entry (NCBI gibbsq 156492) from the This sequence comes from Fig. 2a. | mutation in the glycine receptor 7 (2), 131-135 | | KEYWORDS SOURCE Mus sp. ORGANISM Mus sp. Eukarvota: Metazoa: Chordata: Craniata: Vertebrat | ON GLRA1-inhibitory glycine receptor alpha 1 s brainstem, spinal cord, mRNA, 1407 nt]. N S73717 S73717.1 GI:765206 | \$73717 \$73717 1407 bp mRNA linear |
|---|---|--|--|---|--|---|--|--|---|---|---|--|--|--|--|--|---|--|
| TTCTTTGCTAATGAGAAAG 415 | | | Qy CCTGCAACATCTTCA 235 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 17 21 | gth 1407; ls 57: Gaps 5: | CLOAKDGISVKGANNNNTIN QY NMFYWIIYKIVRREDVHNK" Db | TDWILLEISENGNVLYSIRI DEGGAVQVADGLTLPQFILK DEGGAVQVADGLTLPQFILK DESLITVILSWISFWINMDA Db | Qy EAEAARSAPKPMSPSDFLDK Db TMDYRVNTTI.ROOWNDPRIA | GlyR alpha 1" Qy or alpha 1 subunit Db | Qy wence comes from Db | d" Qy | Qy Db | y of Medicine created this original journal article. | | a > (0) | Qy ata: Futeleostomi: Db | [mice, | ar ROD 17-JUL-2000 |
| | 1370 TTGTCTATAAAGTGCTATGGTCAGAAGATATCCACCA 1406 | 1310 ACACCATCTCCCGGGCTGTCTCCCCTTTCACTTTCCTCAATATCTTCTACTGGG 1369 | 1250 CTCTTCTAAGGGAAGGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTG 1309 | 1193 CAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCC 1249 | 1136 TCATCCAAGAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGG 1192 | 1076 AGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATA 1135 | 1016 GTCTGCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTCTCGTC 1075 | 956 CCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGT 1015 | 896 CTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCT 955 | 836 CCAGCCTACTCATCCTCATCCTGTCCTGGGTCTCCTGGATCAACATGGATGCTGCCC 895 | 776 TCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCC 835 | 716 GGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCA 775 | 656 TGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGC 715 | 596 CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGC 655 | 536 TCCCCATGGACATCCAGACGTGCACGATGCAGCCTTGAGAGCCTCATCCATACTCTGCAGCC 595 | 476 ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTG | GGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGA | 395 TTGACCCATCTATGTTGGATTCCATCTGGAAGCCTGACTTGTTCTTTGCCAATGAGAAGG 454 |

| Oy 2: Oy 2: Oy 2: Oy 2: Oy 3: Oy 3: | SE COUNT IGIN Query Mat Best Loca Matches | FEATURES source gene CDS | LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED |
|--|---|---|--|
| 149 AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC 208 | /note="strychnine binding alpha-1 subunit" /codon_start=1 /product "inhibitory glycine receptor" /db_xref "G1:31851" /db_xref "G1:31851" /db_xref "Sulsa PROT': P23415" /translation "MYSENTLRLYLSGALVFESLAASKEARRASATKPMSPSDFLDK LMGRTSGYDARIREPRECNITALISEARTHEEROWGYVINGLIFINKTURETURETINE LARGEDLECTECHYNTGKFGTCIEARFHLEROWGYVINGLITYLLAISRANONE PRODUCTIVILIMITOSSGERASLEKYSYVKALDIWANCLLEVFSALLEYAANNE VSRQHKELLRERRKRHHKEDEAGEGRENESAYGMGPACLOAKDGISVKGANNSNTIN PRAPAKYGLOTTVLIMITOSSGERASLEKYSYVKALDIWANCLLEVFSALLEYAANNE VSRQHKELLRERRKRHHKEDEAGEGRENESAYGMGPACLOAKDGISVKGANNSNTIN PRAPAKYGLOTTVLIMITOSSGERASLEKYSYVKALDIWANCLLEVFSALLEYAANNE VSRQHKELLRERRKRRHKEDEAGEGRENESAYGMGPACLOAKDGISVKGANNSNTIN PRAPAKYGLOTTVLIMITOSSGERASLEKYSYVKALDIWANCLLEVFSALLEYAANNE VSRQHKELLRERRKRHKEDEAGEGRENESAYGMGPACLOAKDGISVKGANNSNTIN PRAPAKYGLOTTVLIMITOSSGERALEROWGYVIISTRIVKIVRREDVHNQ" 424 a 480 c 407 g 404 t 40.0%; Score 656; DB 9; Length 1715; al Similarity 71.9%; Pred. No. 2.6e-171; 952; Conservative 0; Mismatches 315; Indels 57; Gaps 5; 89 AGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCTCTGATTTCCTAGACA 148 | | HSGLYRA2 H. saplens alpha-1 strychnine binding subunit of inhibitory glycine receptor mRNA. K52009 K52009 K52009: K |
| SULT | , 64 64 64 64 64 64 64 64 64 64 64 64 64 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 |
| | 869 CCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCATCACCACCGTGC 928 | 689 GCCTGACTCTGCCCCAGTTTATCTTGCGGATGAGAAGGATCTAGGCTGTTGTACCAAGC 748 | |

| Ouery Match Best Local Matches 93 Oy 84 Db 84 Oy 144 Oy 204 Oy 204 Oy 264 Ob 264 Ob 324 | CDS CDS BASE COUNT ORIGIN | RNO310837 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE |
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| / Match 39.9%; Score 654.8; DB 10; Length 1359; Local Similarity 70.8%; Pred. No. 5.Se-171; pes 938; Conservative 0; Mismatches 332; Indels 54; Gaps 3; 84 AAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCCAGGCCCATGTCCCCTCTGAATTTCT 143 | /or /db /dc /fu /dc /dc /dc /dc /fu /fu /fu /fu /dx /fu /dx | RNO310837 Rattus norvegicus mRNA for glycine receptor alpha 2 precursor. AJ310837 AJ310837.1 GI:13548660 glycine receptor alpha 2 precursor. Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus 1 (bases 1 to 1359) Beato, M., Groot Kormelink, P.J., Colquhoun, D. and Sivilotti, L.G. Concentration dependence of single channel currents through rat recombinant alpha 1 glycine receptors (published 2 (bases 1 to 1359) Groot-Kormelink, P.J. Direct Submission Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Pharmacology, The School of Pharmacy, 29/39, Brunswick Square, Location/Qualifiers 1 . 1359 1 . 1359 |
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| | D D D D D D D D D D D D D D D D D D D | |
| 1104 AAGCCACAGGCCCAACGCTTCGAGGAAAGTCATCCAAGAAAGTCGTTTCTATTTCCG 1163 | CAAGCACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGCA | 384 GAAGCCAGACCTCTTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGA 443 11 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                       CACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTC
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                                                                            ATACAGTGAGTACCCAGATGATTCCCTGGATTTGGATCCATCGATGCTGGATTCGATTTG
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NDSRLAYSEYEDDSLOLDSSMLDSINKFDLFFANEKGANFHDYTTDNKYLRISKNKY
LYSIRLTLTLSCPMDLKNFPMDVQTCTMQLESFGYTMNDLIFEWLSDGPVQVAEGLTL
PQFILKEEKELGYCTKHYNTGKFTCIDVKFHLERQMGYYLIGWIFPSLIVILSWVSF
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/product="inhibitory
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YAAVNFVSRQHKEFLRLRRRQKRQNKEEDVTRESRFNFSGYGMGHCLQVKDGTAVKAT
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/db_xref="GI:288345"
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/db_xref="taxon:10116"
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| Y Match Local Similarity 70.8%; Pred. No. 6.4e-171; Length 385; Length 3865; Length | 1087 | /organism="Rattus norvegicus" /strain="Wistar" /db_xref="tason:10116" /tissue_type="spinal cord" /de_stage="10 days old" 1. 3865 1. 3865 1. 3865 1. 3865 /gene="NGlyR" 1. 3865 1. 3865 1. 3865 1. 3865 /gene="NGlyR" 1. 3865 /gene="NGlyR" /evidence=experimental 1173. 2551 /gene="NGlyR" | x57281.1 GI:56743 x57281.1 Charlet receptor x64 x x x x x x x x x x x x x x x x x x |
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| Query Match Best Local Similarity 72.6%; Pred. No. 6.2e-171; Best Local Similarity 72.6%; Pred. No. 6.2e-171; Best Local Similarity 72.6%; Pred. No. 6.2e-171; Matches 941; Conservative 0; Mismatches 299; Indels 57; Gaps 5; Oy 116 CCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGGTATG 175 BEST Local Similarity 72.6%; Pred. No. 6.2e-171; Oy 116 CCCAGCCCATGTCCCCCTGATTTCCTAGACCTAACCTTATGGGGACATCTGGGTATG 175 Oy 176 ATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTCTCGACACATCTTCA 235 Oy 176 ATGCCAGGATCAGACCCAACTTTAAAGGTCCTCCTGTGAACGTGAACATCTTCA 235 Oy 158 ATGCCAGGATCAGACCCAACTTTAAAGGTCCTCCTGTGAACGTGAACATCTTCC 217 Oy 236 TCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAACATCTTCTC 295 Oy 296 GGCAACAGCTTTGGTTCTTATCGCCGAGACAACACCTAACAGGTCAACATCTTCCTGA 277 Oy 296 GGCAACAGTTGGAATGACCCACACCATGGACTACAGGGTCAACATCTTCCTGA 277 Oy 296 GGCAACAGTTGGAATGACCCACACCATGGACTACCGGAGAATATCCTGGACC 355 | /strain="Sprague-Dawley males" /db_xref="taxon:10116" /tissue_type="whole brain" /clone_lib="rat brain marathon-ready cDNA" /dev_stage="8-12 weeks" /dev_stage="8-12 weeks" /note="alternative splicing, primary transcript" /note="alternative splicing, primary transcript" /codon_start=1 /evidence=experimental /product="glycine receptor alpha 1 precursor" /protein_id="CAC35978.1" /product="glycine receptor alpha 1 precursor" /product="glycine receptor alph | REFERENCE 1 AUTHORS Beato,M., Groot-Kormelink,P.J., Colquhoun,D. and Sivilotti,L.G. TITLE Openings of the rat recombinant alpha 1 homomeric glycine receptor as a function of the number of agonist molecules bound JOURNAL J. Gen. Physiol. 119 (5), 443-466 (2002) MEDLINE 2197760 REFERENCE 2 (bases 1 to 1350) REFERENCE 2 (bases 1 to 1350) Groot-Kormelink,P.J. TITLE Direct Submission Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Pharmacology, The School of Pharmacy, 29/39, Brunswick Square, London, WCIN 1AX, UNITED KINGDOM COMMENT related splice variants AJ310835 and AJ310836. FEATURES SOURCE (Organisms-Rattus norvegicus" | RESULT 11 RNO310834 LOCUS COUSTITION RATTUS NOTVEGICUS MRNA for glycine receptor alpha 1 precursor, primary transcript. ACCESSION AJ310834 VERSION KEYMORDS ALTINATIVE splicing; glycine receptor alpha 1 precursor. SOURCE ORGANISM Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rattus. Rattus. |
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| Qy 1136 TCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGG 1192 Db 1067 AGGGTGGAAGAGCCGCTTCAACTTCTCCGCCTATGGGATGGGCCCAGCCTGCCT | 713 TTGAGGCCGATTCCACCTGGAACGCCGATGGCTACTACTGCTGCTGCTGCCCGATGCACCTGATCCACCTGATCCACCTGGATGCATGGCTACCTGATCCACATGGATGCATCCACCTGATCCACCTGATCCACCTGATCCACCTGATCCACCTGATCCACCTGATCCACCTGATCCACCTGCCCCCCCC | Db 518 TCCCGATGGATGTACAGTGTATCATGCAAAGCT | Db 278 GGCAGCAGTGGAACCACCCGGTCTCGCCTACAATGAATATCCTGACGACTCTCTGGACC 337 Qy 356 TCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTTGCTAATGAGAAAG 415 |

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glycine receptor alpha 1; GlyRalphal
Rattus norvegicus (strain:Wistar) older than
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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                                                                                                                                                                                              /gene="Gly|
269. .1531
                                                                                                                                                                                                                                                                              /product="glycine receptor alpha 1 precursor"
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/protein_id="BAA00707.1"
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/db_xref="G1:220751"
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TLTLACPMDLKKNFPMNVGYCIMGLESFGYTMNDLIFEWGDGAVQVADGLTLPQFILK
EEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINNDA
APARWGLGITTYLTMTTQSSGSRASLPKVSYYKAIDIWMAVCLLFVESALLEYAAVNNF
                                                                                                                                          /product="glycine receptor alpha
593 c 527 g 469 t
                                                                                                                                                                                                                                                 VSRQHKELLRFRRKRRHHKDDEGGEGRFNFSAYGMGPACLQAKDGISVKGANNNNTTN
PAPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10116"
/tissue_type="spinal cc
/dev_stage="older than
/note="314 bp upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="GlyRalphal"
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                                                                                                                                                                                /gene="GlyRalphal"
                                                                        39.9%;
                                                                                                                                                                                                               "GlyRalphal"
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Rodentia;
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                                                    Score 654.6; DB 10;
Pred. No. 6.6e-171;
0; Mismatches 299;
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 CCAAGGATGGCATCTCTGTCAAGGGTGCCAACAACAACAACACCAC
                                    CAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTC
                                                                      AGCATAAAGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATA
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Вb

510 CCTATCTCCTTCAGATTTCTTGGACAAGTTAATGGGAAG

| ORIGIN Query Match Query Match 39.6%; Score 650.2; DB 9; Length 1857; Best Local Similarity 70.1%; Pred. No. 1.Le-169; Best Local Similarity 70.1%; Pred. No. 1.Le-169; Matches 943; Conservative 0; Mismatches 348; Indels 54; Gaps 3; Matches 943; Conservative 0; Mismatches 348; Indels 54; Gaps 3; Qy 63 CCTCCTCAGGGGCGTTTCTGGCAAAAAAAAAAAAGAGGAACCAAACCAAAGGGTCCCAGCC 122 | /COGON_SCATC#1 //COGON_SCATC#1 //product="inhibitory glycine receptor" //db_xref="swiss-profus" //db_xref="swiss-pro | X X (0.X X X X X X X X X X X X X X X X X X X | glycine re glycine re Homo sapid Homo sapid Eukaryota, Manmalia; 1 (bases Grenningles, Siddique, Alpha sub structures tructures tructures EMBO J 9 90183975 | Db 1491 TCATCTACAAGATCGTCCGGAGAGAGGACGTCCACAA 1527 RESULT 13 HSGLYRA1 LOCUS DEFINITION H.saptens alpha-2 strychnine binding subunit of inhibitory glycine receptor mRNA. ACCESSION X52008.1 VERSION X52008.1 GI:31848 | Qy 1252CTTCTAAGGAAGAGAAACCACGCGAAACTCTACGTGACCCAAGAGAATTG 1309 |
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| Oy 1083 AGAATTCATACGACTTCGAAGAAGGCAGAGGCCCAACGCTTGGAGGAAGATATCATCCA 1142 | Db 1185 GCTTATAGTAGCTACCACCAGGATGACCACCAGAGTTCAGGCCTCTGCT 1244 Qy 903 TGTGGGCCTGGGCATCACCACCATGACCACCAGAGCTCTGGCTCCCGGGC 962 | 101 101 111 111 111 111 111 111 111 111 | 483 870 930 603 965 | 690 363 750 423 | Qy 183 GATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTCACCC, |

| Qy 89 Db 299 | Query Match Best Local Matches 95 | BASE COUNT ORIGIN | | | | gene | сe | r | MEDLINE PUBMED REFERENCE AUTHORS | | REFERENCE AUTHORS | KEYWORDS SOURCE ORGANISM | ITION SION ON | RESULT 14 AF268375 LOCUS | Qy 1383 Db 1716 | Qy 1323 Db 1656 | Db 1596 |
|--------------------------|---|--|---|---|---|---|--|--|---|--|---|--|--|--|--|---|---------|
| AGGAAGTCAAATCTGGAACCAAGG | Query Match 39.4%; Score 646.8; DB 4; Length 1744; Best Local Similarity 71.2%; Pred. No. 9.6e-169; Matches 956; Conservative 0; Mismatches 317; Indels 69; Gaps 5; | ANNSNTMPPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVR REDVHNQ* 396 a 508 c 451 g 389 t | TLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEQGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTC1EARFHLERQWGYYLLDWY1FSLLIVILSWISFWINNDA APARVGLGITTVLTMTTQSSGSRALPKVSYVKAIDIWAAVCLLFVFSALLEYAAVNF VSRQHKELLRFRRRRHHKSPMLNLFQEDEAGEGRFNFSAYGMGPACLQAKDGISVKG | /db_xref="GI:10180959" /translation="Mysfwilklylmetivffslaaskeaeaarsaskpmspsdfldk /translation="mysfwilklylmetivffslaaskeaeaarsaskpmspsdfldk LMGRTSGYDARIRPMFKGPPVMVSCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLA YMEYPDDSLDLDPSMLDSTWKPDLFFANEKGAHFHEITTDNKLLRISRNGAVLYSIRI YMEYPDDSLDLDPSMLDSTWKPDLFFANEKGAHFHEITTDNKLLRISRNGAVLYSIRI | /note="Glralins; alternatively spliced" /codon_start=1 /product="glycine receptor alpha 1 subunit" /protein_id="AAG14346.1" | 1. 1/44 /gene="Glral" 229. 1602 /gene="Glral" | Location/Qualifiers 1. 1744 /organism="Bos taurus" /db_xref="taxon:9913" | biology Pr a Street, | 21109390 11178872 2 (bases 1 to 1744) Pierce,K.D., Handford,C.A., Morris,R., Vafa,B., Dennis,J.A., | Healy, P.J. and Schotled, P.K. A nonsense mutation in the alphal subunit of the inhibitory glycine receptor associated with bovine myoclonus Mol. Cell. Neurosci. 17 (2), 354-363 (2001) | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos. 1 (bases 1 to 1744) Pierce, K.D., Handford, C.A., Morris, R., Vafa, B., Dennis, J.A., | vetazoa; | <pre>us glycine receptor alpha 1 subunit (Glra1) ernatively spliced1 GI:10180958</pre> | AF268375 1744 bp mrna linear mam 22-may-2001 | GCTATGGTCAGAAGATATCCACCAG 1407 | GGCTGTCTTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGT 1382 | |
| da | D Dy | Db | Qу | Qy Db | Qy Db . | Qу | Дb | Qу | Qу | Qу | Qy Db | Qу | Qу | Qy Db | Qy Db | Qу | Db |
| 1131 | 4 4 | 9 ATGCTGCCATAAATTTTGTTTCTCG | 989 AGGCAATCGACATCTGGATGGCTGTGTGTGTGTTTGTGTTCGCTGCCTTGCTGGAGT | 929 TCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGA | 869 CCTTCTGGATCAACATGGATGCCCCCCTGCCCCTGTGGGCCTGGGCCTCACCACCGTGC | 809 GCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCCTCATCCTGGCTCT | 4 9 | 689 GGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGC | 7 | 569 TTGACAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCACTTGCCTACA | 9 9 | 449 AGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTT | 389 CAGACCTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACACACA | 329 GAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGC | 269 TGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACC | 209 CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA | |

| Query Best 1 | BASE COUNT ORIGIN | | | | | gene CDS | SQ | REMARK FEATURES | JOURNAL MEDLINE PUBMED | REFERENCE AUTHORS TITLE | SOURCE ORGANISM | ACCESSION VERSION KEYWORDS | S73718 LOCUS DEFINITION | | Qy | p 49 | Оу | Qу |
|---|-----------------------------|--|---|---|--|--|---|--|---|--|--|---|--|--|--|---|--|---|
| Query Match 39.4%; Score 645.4; DB 10; Length 1431; Best Local Similarity 71.9%; Pred. No. 2.3e-168; | UNT 355 a 411 c 336 g 329 t | EEKOLEKYCTKHYNTGKETGLEARFHLEREQMGYYLLQWYDIGGAVQVADGLTLPOYILK EEKOLEKYCTKHYNTGKETGLEARFHLEREQMGYYLLQWYIPSLLIVILSWISFWINMDA APARVGLGITTVLTMTTQSSGSRASLPKVSYVKALDIWMAVCLLEVESALLEYAAVNF VSRQHKELLRERRKRRHHKSPMLNLFQDDEGGEGRFNFSAYGMGPACLQAKDGISVKG ANNINTTUPPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVR | /db_xref="GI:9247216" /translation="MYSFNTULRETIVFFSLAASKEAEAARSAPKPMSPSDFLDK /translation="MYSFNTULRETIVFFSLAASKEAEAARSAPKPMSPSDFLDK LMGRTSGYDARIRPMFKGPPVNVSCNIFINSEGSTAETTMDYRVNIFLRQQWNDPRLA YNDYPDDSLDLDFSMLDSTWKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRI | <pre>/codon_start=1 /product="inhibitory glycine receptor alpha 1 subunit long form" /protein_id="AAB32158.2"</pre> | /gene="Giral" /note="alternatively spliced; This sequence comes from Fig. 2a and 2b; conceptual translation differs from that in published reference; GLRA1 protein; GlyR alpha 1" | | source. 11431 /organism="Mus sp." /db_xref="taxon:10095" /tissue_type="brainstem and spinal cord" | GenBank staff entry {NCBI g This sequence Loca | inhibitory glycine receptor in the spasmodic mouse Nat. Genet. 7 (2), 131-135 (1994) 95004575 7920629 | 1 (bases 1 to 1431) Ryan,S.G., Buckwalter,M.S., Lynch,J.W., Handford,C.A., Segura Shiang,R., Wasmuth,J.J., Camper,S.A., Schofield,P. and O'Connu A missense mutation in the gene encoding the alpha 1 subunit of the series of the ser | _ | ON 573718 S73718.1 GI:765208 | | 1574 TCCGCAGGGAGGTCCACAA 1595 | TATGGTCAGAAGATATCCACCA 1406 | 1325 CTGTCTTCCCTTTCCACATCCTCAATATCTTCTACTGGGTTGTCTATAAAAGTGC 1384 | 1265 GAGAAACCACGGGGAAACTCTACGTGGACTGAGGCCAAGAGAATTGACACCATCTCCCGGG 1324 | 1208 CAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCTCTTCTAAGGGAAG 1264 |
| Db | Db | Db Dy | Ωy | Db | Qγ | Db | Qγ | Qy Db | Qy Db | Qy | Qy | Ф | ДŊ | Qy Db | Db . | Db | . Фр | Matches Qy |
| 1118 AACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTGG 1177 | | 1016 GTCTGCTCTTTGTGTTCGCTGCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTC 1075 | CCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGT | 896 CTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCACAGAGCTCTGGCT 955 | 836 CCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCC 895 | 7/6 TCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATCTACATCC 835 | GGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCA | 656 TGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCCCAGTTTATCTTGC 715 | 596 CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGC 655 | 536 TCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCC 595 | 476 ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCCTG | 416 GGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGA 475 | TCGATCCCTCCATGCTGGACTCTATCTGGAAGGCAGACCTCTTCTTTGCTAATGAGAAAG | 296 GGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTCTGGACC 355 | 230 ICANCHOTTICAUCTCUCTCACCANGACCACTIGGACTACCGGGTGAATGTCTTGC 295 + + + + + + | ACGCCAGGATCAGGCCCAACTTTAAAGGTCCTCCTGTGAACGTAAGTTGCAACATCTTCA | 155 CCAAGCCTATGTCACCCTCGGACTTCCTGGATAAGCTCATGGGAGGAGGACTCTTGGGTATG 214 176 ATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACATCTTCA 235 | hes 945; Conservative 0; Mismatches 301; Indels 69; Gaps 5; 116 CCCAGCCCATGTCCCCCCTCTGATTTCCTAGACAACTTTATGGGGGGGAACATCTGGATATG 175 |

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| | | | 1310 AGAGAGCCAAGAAGATCGACAAGATATCTCGCATCGGTTTCCCCATGGCCTTCCTCATCT 1369 | 1292 ACTGAGCCAAGAGAATIGACACCATCTCCCGGGCTGTCTTCCCTTTCACTTTTCCTCATCT 1351 | 1250 CCACTAACCCGCCTCCTGCGCCATCCAAGTCCCCGGAGGAGATGCGGAAACTCTTCATCC 1309 | 1235 CCCAACCTCCAGCCCCTTTTTTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGG 1291 | 124 | 1178 GCCACTGCCTGCAGGCAAGAGATGGAAGGTCCAATGGAAGGTTCTGGCATTTATAGTC 1234 |
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                                                                                   for ataxia
                                                  WO 0058461-A 1 05-OCT-2000, HOERBRAND GUDRUN (DE) Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
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1. .1254
                                                                                                                                       construct.
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SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSITKTTMDYRVNVFLRQOW

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LYSIRITILISCLMDLKMFPMDIOTCTMQLERFGYTMKDLVFEWLEDAPAVQVAEGLT

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EYAAINFVSRQHKEFIRLRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEG

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/codon_start=1
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Groemer, T.-W., Becke
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Mammalia; Eutheria;
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1. .1251
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/note="mmGlra4"
                                                            /organism="Mus musculus"
/strain="B6C3/Fe"
                                       /chromosome="X"
                                                  /db_xref="taxon:10090"
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                    LysaspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluVal
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|AGGATCTAGGGTATTGTACCAAGCACTACAATACAGGAAAATTCACTTGCATTGAGGTA
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TETTMOYRVNVELROGMUDPRLAYREXPDDSLDLNESMLESIMKPDLFFANEKGANFH
EVTTDNKLLRIFKNGNVLYSIRLTLILSCPMDLKNEFMDIQTCTMQLESFGYTMNDLM
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IQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLFKVSYVKA
IDIWMAVCLLFVFAALLEYAAVNFVSRQHKEFWRLRRORRQRMEEDIIRESREYFRG
YGLGHCLQARDGGPMEGSSIYSPQPPTPLLKEGETMRKLYVDRAKRIDTISRAVFPFT
FLVFNIFYWYVXVLRSEDIHQAL"
a 334 c 281 g 332 t
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/note="ligand-gated ion channel"
/codon_start=1
/product="glycine receptor alpha
/protein_id="AAL69899.1"
/db_xref="GI:18448711"
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94.36%
91.79%
83.75%

    AGCTTTGGCTACACCATGAATGACCTCATGTTTGAGTGGCTAGAAGAT

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Cypriniformes; Cyprinidae; Dan
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25 rue du Dr Ro
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                                /gene="glyR alpha"
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                                                     /gene="glyR alpha"
<1. .519
                                                                                 /organism="Danio rerio"
/db_xref="taxon:7955"
/tissue_type="brain"
/dev_stage="adult"
                                                                                                                           1. .2045
                                                                                                                                 25 rue du Dr Roux,
Location/Qualifiers
           /gene="glyR alpha"
/codon_start=1
   /product="glycine receptor
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eptor alphaZ2
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INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLIVFAALLEY
AAVNFVSRQHKEFIRLKKQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKDGTAVEGS
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DFLDKLMGRTSGYDARIADHFKOFPVNVTCNIFINSFGSITETTMOYRLNVFLRQQWN
DPRLAYSEYDDASLDLDSMLDSIWKPDLFFANEKGANFHEVTTONKLLRIFQNGNVL
YSIRLTLILSCPMDLKNFPMDIQTCTMQLESFGYTMNDLIFEWLSDNPVQVADDLTLP
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/gene="glyR alpha"
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                                                                                                                                                                                          EMBO J. 9
                                                                                                                                                                                                                                    Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1857)
Grenningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H. Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization of
                                                                                                                                                                                                        the corresponding genes
EMBO J. 9 (3), 771-776 (1990)
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                               /gene="GLYRA1"
388. .1746
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="brain"
/dev_stage="fetal"
/note="strychnine binding alpha-2 subuni
                                                                                                                                              Cocation/Qualifiers
l. .1857
                /gene="GLYRA1"
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binding subunit of inhibitory glycine
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AspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLys
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                                                              CCA---GTGCAAGTTGCTGAAGGATTGACCCTGCCCCAGTTTATTTTTGAAAGAAGAAGAAG
                                                                                ProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLys
                                                                                                                                                           LeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAla
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SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSVTETTMDYRVNIFLRQQW
NDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHDVTTDNKLLRISKNGKV
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PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
WINMDAAPARVALGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLE
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/db_xref="SWISS-PROT:P23416"
/db_xref="SWISS-PROT:P23416"
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                                                                                                                                                                                                                Direct Submission
Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Pharmacology, The School of Pharmacy, 29/39, Brunswick Square, London, WCIN IAX, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1359)
Beato, M., Groot-Kormelink, P.J., Colquhoun, D. and Sivilotti, L.G.
Concentration dependence of single channel currents through rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa;
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AJ310837
AJ310837.1 GI:13548660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSer 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGATGCTATCAAGAAGAAGTTTGTGGAC 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProMetGluGlySerGlyIleTyrSer---ProGlnProProAlaProLeuLeuArgGlu 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTCGTTTTAATTTTAGCGGTTATGGGATGGGTCACTGCCTCCAAGTGAAAGATGGAACA 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCCAAAGGTCTCCTATGTAAAAGCGATTGACATCTGGATGGCGGTGTGCCTTCTGTTT
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                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1359)
                                                          /tissue_type="whole brain"
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1. 1359
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  /codon_start=1
/evidence=experimental
                                                                                                                                                                           /organism="Rattus norvegicus"
                                        /function="ion channel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
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GTGCTCTACAGTATTAGACTCACCTTGACTTTATCCTGTCCCATGGACCTGAAGAACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsn 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValLeuLeuArgValAlaLeuAlaLysGlu---GluValLysSerGlyThrLysGlySer
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                                                                                                    CTAGTGAACATTTTGACAGCCTTGTTTGCATTTTTCTTA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCACTTCAGGGAAGCATTCTGCAAAGACCATGACTCCAGGTCTGGAAAACATCCCTCG 117
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/braref="GI:3548661"
/db_xref="GI:3548661"
/translation="mangluvalitalfaffication: growth of the product of the pro
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| /GD_XIGH SWIJS FROM SEARCH SEARCH FEARFCKDHDSRSGKHPSQTLSP /translation-mwnRQLVNITALFAFFLGTNHFREAFCKDHDSRSGKHPSQTLSP SDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIF INSFGSVTETTMDYRVNIFLRQQW NDSRLAYSEYDDDSLILLDSMLDSIWKDDIFFANFKGANFHDVTTDNKILBTKNGKV |
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| CDS 5521910 |
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| OURNAL FEBS Le |
| <pre>lternative splicing gener f the inhibitory glycine</pre> |
| Betz,H. |
| Manifet.V. Malosio.M.L. Schmieden |
| dentia; Sciurognathi; Muridae; Murinae; |
| NISM Rattus norvegicus Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi |
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| RESULT 7 |
| Db 1204AAAGATGCAGATGCTATCAAGAAGATTTGTGGAT 1239 |
| Qy 419 LeuArgGluGlyGluThrThrArgLysLeuTyrValAsp 431 |
| Db 1153 GATGGTACAGCTGTCAAGGCTACACCTGCCAACCCCACTTCCGCAACCCCCCA 1203 |
| Qy 400 AspGlyGlyProMetGluGlySerGlyIleTyrSerProGlnProProAlaProLeu 418 |
| Db 1093 ACTCGTGAAAGCCGTTTTAACTTCAGCGGTTATGGGATGGGTCACTGCCTCCAAGTGAAA 1152 |
| Qy 380 IleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHiSCysLeuGlnAlaArg 399 |
| Db 1033 CACAAGGAGTTCCTTCGTCTCCGGAGACAGAAGAGGCAGAATAAGGAAGAAGATGTT 1092 |
| Qy 360 HisLysGluPheIleArgLeuArgArgGlnArgArgGlnArgLeuGluGluAspIle 379 |
| Db 973 CTTCTGTTTGCTGCTTGCTGCCTTACTGGAATATGCAGCAGTGAACTTTGTCTCCCAGGCAA 1032 |
| Qy 340 LeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln 359 |
| Db 913 AGGGCATCTCTGCCAAAGGTCTCATATGTGAAAGCAATTGACATCTGGATGGCAGTGTGC 972 |
| Qy 320 ArgAlaSerLeuProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCys 339 |
| Db 853 GCCAGGGTTGGCCTTGGCATCACAACCGTCCTGACAATGACTACCCAGAGTTCAGGTTCC 912 |
| Qy 300 AlaArgValGlyLeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySer 319 |
| Db 793 AGCCTGCTGATAGTCATTTTGTCCTGGGTCTCCTTTTGGATAAACATGGATGCAGCTCCT 852 |
| Qy 280 SerLeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaPro 299 |
| Db 733 GAGGTCAAGTTTCACCTGGAACGCCAGATGGGCTATTATTTGATCCAGATGTATATCCCC 792 |
| Oy 260 GluvalLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIlePro 279 |
| Db 673 GAAGAGAACTTGGCTATTGCACAAAGCATTACAACACTGGCAAGTTTACCTGCATT 732 |
| Qy 240 AspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIle 259 |
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                                                          GluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArg
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PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQWIPSLLIVILSWVSF
WINMDAAPARVALGITTVLTMTTQSSGSRASLFKVSYVKAIDIMMAVCLLFVFAALLE
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PANPLPQPPKDADAIKKKFVDRAKRIDTISRAAFPLAFLIFNIFYWITYKIIRHEDVH
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                                               -GTACAAGTTGCTGAAGGACTCACCCTGCCTCAGTTTATTTTGAAA
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AUTHORS
TITLE
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2 (bases 1 to 3865)
Akagi, H., Hirai, K. and Hishinuma, F.
Cloning of a glycine receptor subtype
spinal cord during a specific period o
FEBS Lett. 281 (1-2), 160-166 (1991)
                                                                                                                                                                                                                                                                                                                                           x57281.1 GI:56743 glycine receptor; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                               Rat NGlyR mRNA
X57281
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                                               /strain="Wistar"
/db_xref="taxon:10116"
/tissue_type="spinal co:
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1. 3865
 /gene="NGlyR"
/evidence=experimental
                                                                                                            /organism="Rattus
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sdfluklmgrisgydarirphrkgppvnvtchifinsfgsvptetmdyrnvhtelrqom
NDSRLAYSEYPDDSLDLDPSMLDSIMKPDLFfahaEkgahfDVTTDNKLLRISKNGKV
LYSIRLTLTLSCPMDLKHFPMDVQTCMQLESFGYTMNDLIFEMLSDGPVQVAEGLTL
LYSIRLTLTLSCPMDLKTPMDVQTCMQLESFGYTMNDLIFEMLSDGPVQVAEGLTL
PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSF
WINMDAPARVALGITTVLTMTGSSGSRASJPKVSYYKAIDIMMAVCLLFVFAALLE
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PANPLPQPPKDADAIKKKFVDRAKRIDTISRAAFPLAFLIFNIFYWITYKIIRHEDVH
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/db_xref="SWISS-PROT:P22771"
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/codon_start=1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3069)

Nikolic, Z., Laube, B., Weber, R.G., Lichter, P., Kioschis, P.,
Poustka, A., Mulhardt, C. and Becker, C.M.
The human glycine receptor subunit alpha3. Glra3 gene structure,
The human glycine receptor subunit alpha3.
                                                                                                                                chromosomal localization, and functional characterization alternative transcripts
J. Biol. Chem. 273 (31), 19708-19714 (1998)
98344067
                                                        Direct Submission
Submitted (17-MAR-1997) Biochemistry, University
Erlangen-Nuremberg, Fahrstr. 17, Erlangen 91054,
                                                                                                     Nikolic, Z.
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/organism="Homo sapiens"
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                                                     SerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAsp
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Submitted (30-MAR-2001) Groot-Kormelink P.J., Departmen
Pharmacology, The School of Pharmacy, 29/39, Brunswick
London, WCIN 1AX, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                            glycine receptor
Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus mRNA
AJ310838
AJ310838.1 GI:13548662
                                                                                                                                                                                                                       Groot-Kormelink, P.J.
                                                                                                                                                                                                                                       Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                              Beato,M., Groot-Kormelink,P.J., Colquhoun,D. and Sivilotti,L.G. Concentration dependence of single channel currents through rat
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                recombinant alpha
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                                                     /tissue_type="whole brain"
/clone_lib="rat brain marathon-ready
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                                                                                            /strain="Sprague-Dawley males"
/db_xref="taxon:10116"
/codon_start=1
/evidence=experimental
                           /function="ion channel"
                                        /dev_stage="8-12
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                                                                                                     TyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAla
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                  GAAGGACTCACTTTGCCTCAATTTCTGTTGAAAGAAGAAAAAGATTTGCGATACTGCACT
                                                                                     TACACGATGAATGATCTCATTTTCGAATGGCAAGATGAAGCACCA---
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/translation="MMWIRLESCSGISFRIMAHVRHFRTLLSGFYFWEAALLLSLVAT/
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TTDNKLLRIFKNGNVLYSIRLFLLTLSCEMDLKNFPMDVGTCHQLESFGYTMNDLIFE
WQDEAPPQVAREGLTLPGFLLKEEKDLRYCTKHYNTGKFTCIEVRFHLERQMGYYLIQM
YIPSLLYVLSWYSFWINNDAAFARVALGITTVLTMTTOSSGSRASLERVSYVKAIDI
YIPSLLYVLSWYSFWINNDAAFARVALGITFNLTMTVGSKGSRASLERVSTYRFSDTDDEV
RESRFSFTAYGMGPCLQAKDGVPKGPHAYQVMPKSADEMRKVFIDRAKKIDTISRA
RESRFSFTAYGMGPCLQAKDGVPKGPHQQD"
a 320 c 324 g 394 t
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/protein_id="CAC35982.1"
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MEDLINE
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                                                   CDS
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N Rat inhibitory glycine receptor alpha subun.

M55250 M38385

M55250.1 GI:204882

Inhibitory glycine receptor.

Rat (strain wistar) adult brain, cDNA to mR

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Metazoa; Chordata; Craniata; Ver
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Kuhse, J., Schmieden, V. and Betz, H.

Identification and functional expression of subunit of the inhibitory glycine receptor J. Biol. Chem. 265 (36), 22317-22320 (1990) 91093073
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                                                                                /db_xref="taxon:10116"
/clone="pGR48-alpha-3"
/tissue_type="brain"
/dev_stage="adult"
1. . 2413
                                                 /gene="inhibitory glycine 400. .1794
 /product="inhibitory
                              /gene="inhibitory
                                                                                                                                                                  /strain="Wistar"
                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                              glycine
 glycine receptor
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                                                CAACTCGAA-
                                                                       GlnLeuGluSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerValGly
                                                                                                 ACACTCTCTTGTCCAATGGATCTCAAGAATTTCCCAATGGATGTTCAAACATGCATAATG
                                                                                                                         IleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMet
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 TACACGATGAATGATCTCATTTTCGAATGGCAAGATGAAGCACCA - - -GTACAAGTGGCT
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DELDKLMGRTSGYDARIRPNEKGPPVNVTCNITINSFGSIAETMDYRVNIFLRQKWN
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QFLLKEEKDLRYCTKHYNTGKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVSFW
INMDAAPARVALGITTVLTMTTQSSGSRASLERVSYVRAIDIMMAVCLLFVESALLEY
AAVNETSRQHKELLRFRRKKNENETARALEKFYRFSDTDDEVRESRLSETAYGNGFCL
QAKDGVVPKGPNHAVQVMPKSADEMRKVFIDRAKKIDTISRACFPLAFLIFNIFYWVI
YKILRHEDIHHQQD"
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/db_xref="GI:204883"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1715)

Grenningloh,G., Schmieden,V., Schoffeld,P.R., Seeburg,P.H., Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H.

Alpha subunit variants of the human glycine receptor: primary structures, functional expression and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.sapiens alpha-l
                                                                                                                                                                                             the corresponding genes EMBO J. 9 (3), 771-776
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/chromosome="X"
/map="xp21.1 - -p22.1"
/tissue_type="brain"
/dev_stage="fetal"
                                                                                                                     Location/Qualifiers
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                                                                                                              LysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSerSerIleLeu
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PPPAPSKSPEEMRKLFIQRAKKIDKISRIGFPMAFLIFNMFYWIIYKIVRREDVHNQ"

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/db_xref="GI:31851"
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297. .1646
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Bos taurus glycine r
cds, alternatively s
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                                              Direct Submission
Direct Submission
Submitted (17-MAY-2000) Neurobiology Program, Garvan Institute
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Mammalia; E
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11178872
                                                                                                                                                            A nonsense mutation in the alphal subunit of receptor associated with bovine myoclonus Mol. Cell. Neurosci. 17 (2), 354-363 (2001)
                                                                                              Healy, P.J. and Schofield,
                                                                                                           Pierce, K.D.,
                                                                                                                                                                                                       Pierce, K.D., Handford, C.A., M. Healy, P.J. and Schofield, P.R.
                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
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 /organism="Bos taurus"
/db_xref="taxon:9913"
                                        Location/Qualifiers
                                                                                                                                                                                                                                                              ; Metazoa; Chordata; Craniata; Vertebrata; Eute
Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                                                                                                                                                    MetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProVal
                                                    SerSerIleLeuCysSerProLeuProSerLeuSerLeuSerValGlyTyrThrMet
                                                                                                                                    CTGAGGATCTCCCGGAACGGGAATGTCCTCTACAGCATTAGGATCACCCTGACATTGGCC
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                                                   Direct Submission
Direct Submission
Submitted (21-MAR-2001) Biochemistry,
Submitted (71-MAR-2001) Biochemistry,
Submitted (71-MAR-2001) Biochemistry,
                                                                                                                                                                                                                                                          complete
AF362764
                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Cran
Eukaryota; Betheria; Rodentia; Sciu
1 (bases 1 to 1392)
Noegel,S., Becker,C. and Becker,K.
Different glycine receptor isoform
                                                                                               2 (bases 1 to 1392)
Noegel, S., Becker, C.
                                                                                                                      Unpublished
                                                                                                                                   cerebellum
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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SIRLTLTLSCPMDLKNFPMDVQTCIMQLEFTMNDLIFENGDENTESHTLIFNFSFMLEYA
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                                                                                 Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1628)
                                                                                                                                                                            Danio rerio mRNA for glycine
                                                                                                                                                       AJ005812.1 GI:3378595
alphaZ1 subunit; glyci
2 (bases 1 to 1)
David-Watine, B.,
                                   Direct Submission
Submitted (27-APR-1998)
U261 - Institut Pasteur,
                         FRANCE
                                                                      David Watine, B
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| JOURNAL DOUBLE LOCALION/Qualifiers ### SOURCE 1.1528 1.1528 2.1628 2.1628 2.1628 Conservative Conserv |
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| LDKLMGK RLAYSEY IRITLVL IRITLVL ILIKEEKD MDAAEPEKD MDAAEPEKD MDAAEPEKD VWFIARQ PTSTNPP Q"" CA 179 CA 179 CA 179 CA 179 JI |

| | uLeuArgGluGlyGluThrThrArgLysLeuTyrVal 430 | 418 1269 | Ф |
|-------------|--|---------------|----------|
| 418 1268 | ArgAspGlyGlyProMetGluGlySerGly-IleTyrSerProGlnProProAlaProLe::: :::: ::: AAAGACGGCATGGCAATCAAGGGCAACAACAACACGCGCCCCCCCC | 399 1209 | Дy |
| 398 1208 | IleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAla ::: ::: | 380 1149 | dd |
| 379 1148 | HistysGluPheIleArgLeuArgArgArgGlnArgArgGlnArgLeuGluGluAspIle | 360 · 1095 | Фр |
| 359 1094 | LeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln ::: ::: | 340 1035 | Qy Db |
| 339 1034 | ArgalaSerLeuProLysValSerTyrValLysAlaIleAspileTrpMetAlaValCys | 320 975 | ОУ ДЪ |
| 319 974 | AlaArgValGlyLeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySer | 300 . 915 | Qу Дъ |
| 299 914 | SerLeuLeuIleVallleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaPro | 280 855 | Фр |
| 279 854 | GluvalLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIlePro ::: | 260 795 | Фр |
| 259 794 | AspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIle::: | . 240 735 | Оу |
| 239 734 | GluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArg ::::: GATGAGAAAGGGAGCCGTGCAGGTAGCAGATGGACTGACGTTACCTCAGTTTATATTGAAG | 220 675 | Qу Дъ |
| 219 674 | LeuProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeu | . 636 | QУ |
| 199 635 | ProMetAspileGinThrCysThrMetGinLeuGluSerSerSerIleLeuCysSerPro | . 180 600 | Qу |
| 599 | GTTTTATACAGTATAAGAATAACACTGGTTCTGGCCTGCCCCATGGACCTGAAGAATTTC | 540 | DЬ |

Search completed: July 1, 2003, 00:16:14
Job time: 3575.13 secs

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Minimum DB seq
Maximum DB seq
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-DB=M_Genneseq_10102 -OFMT=fasta_p -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LCCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEXH=0 -MAXLEN-2000000000
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-DEV_TIMEDUT=120 -MARN_ITMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 AAD33667

AAD33667 standard; cDNA; 1874 BP

ALIGNMENTS

01-JUL-2002 (first entry)

Human TRICH-22 cDNA.

depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease; cell proliferated disorder; infertility; arteriosclerosis; gene therapy; Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;

myasthenia gravis; multiple sclerosis; acquired immune deficiency syndrome; ir

immunological disorder;

metabolic

disorder; hypertension;

scleroderma

Human; transporter and ion channel; TRICH-22; transport disorder; angina; amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer; cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;

SUMMARIES

| 45 | 44 | ٠ د د | 4 1 | | | | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | | 15 | 14 | | 12 | 1 ; | 10 | ۰ | ω | 7 | σ | տ | 4 | w | N | 1 | No. |
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| | 690 | 4 0 4 | 97. | | 98. | 712 | 712 | 715 | 717 | 717 | 717.5 | 718 | 719 | | 720 | 7 | | 724 | 724 | | 25 | 5 | 726 | 28. | 728.5 | | 31 | - | | 73 | 37 | 42 | ٠. | 5 | 2 | 4 | 75 | | 761 | 87 | | | 16 | Score |
| 30.5 | | | | | | _ | 1. | 31.7 | 31.8 | 31.8 | | 31.9 | 31.9 | - | 2 | | 32.0 | 32.1 | | 32.2 | | | 32.2 | 32.3 | 32.3 | 32.4 | 32.5 | 32.5 | 32.5 | 32.7 | 2 | ω: | 33.0 | . س | س | ω | ω · | ω | 33.8 | 38.7 | 43.7 | 5 | 6 | Query Match |
| 97 | 87 | 1879 | 59 | 69 | 64 | 98 | 98 | 49 | 1491 | 1491 | 1823 | 2066 | 3598 | 3442 | 2066 | 2066 | 3619 | 1657 | 1657 | 1519 | 1766 | 1766 | 2066 | 1844 | 1640 | 2340 | 3958 | 1368 | 1614 | 1614 | 1614 | 2289 | 2138 | 1197 | 1197 | 1609 | 4621 | 2400 | 39796 | 2404 | 657 | 1600 | | Length |
| 21 | 22 | 4 C | 24 | 22 | 22 | 15 | 14 | 23 | 20 | 17 | 19 | 21 | 22 | 22 | 21 | 21 | 23 | 19 | 19 | 20 | 22 | 22 | 21 | 20 | 24 | 23 | 17 | 20 | 24 | | | | | | | | | | | | | 21 | | DB |
| AAZ44049 | AAD04275 | ABL5/052 ABD04374 | ABI99308 | AAI58254 | AA160040 | AAQ69143 | AAQ33131 | ABL18879 | AAV84685 | AAQ99330 | AAX16065 | AAZ44047 | AAD21372 | 37 | AAZ44046 | AAZ44045 | ABL13035 | AAV55008 | AAV55007 | AAV64373 | AAD04277 | AAD04276 | AAZ44048 | AAV64372 | AAD26938 | ABL16609 | AAT43596 | AAX24372 | AAD22071 | AAD22070 | AAD22072 | AAD21396 | AAD21395 | AAD22082 | 213 | 2693 | 2693 | 2139 | 168 | 9925 | 2572 | C616 | AAD33667 | ID |
| elanogaster | Long form of S. am | form of s | ischaemic | | | GABA recep | GABA-A receptor be | phila melan | t GABA re | GABA receptor subu | | D. melanogaster GA | vari | | melanogaster | a | ophila | gated | gated | -gated | t form | ort form | ₽ | Q. | | Drosophila melanog | ļ | Cat flea qlutamate | varia | ۲ | Dermacentor variab | sanguineus | sanguineus | sanguineus | sanguineus | liothis sp. | eliothis vir | sanquine | eotide seque | ischaemic | ABA-A receptor b | equence en | man | ption |

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mycarditis, prostate cancer, cardiac disorders associated with

Ctransport e.g. polymyositis, bradyarrythmia, dermatomyositis, angina,

Cneurological disorders associated with transport e.g. amnesia, bipolar

Cdisorder, depression, Tourette's disorder, schizophrenia, other disorders

Cdisorder, depression, Tourette's disorder, schizophrenia, other disorders

Cdisorder, depression, Tourette's disorder, schizophrenia, other disorders

Cdisorder, depression, Tourette's disorder, scikle cell anaemia,

Cdisorder, cushing's disease, infertility, hyperglycaemia, hypoglycaemia,

Cgoitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell

Cproliferated disorders include cancer, actinic keratosis, cirrhosis,

Carteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.

Clisease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's

Cdisease, multiple sclerosis, dementia and other extrapyramidal disorder,

Controller, prion disease, metabolic disease of the nervous

System and other developmental disorders of the central nervous system,
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Reddy R,
reene BD, Sa,
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25-AUG-2000;
31-AUG-2000;
                                                                                                                                                                                                                                                                                                     designated TRICH and nucleic acid molecules encoding such polypeptides TRICH sequences are useful for diagnosis, treatment and prevention of transport, muscle, neurological, immunological and cell proliferative disorders. Transport disorders include akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, diabetes mellitus, diabetes inslidus, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection; epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease; emuscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human transporters and ion channels polypeptides and polynucleotides for diagnosing, preventing or treating t neurological, muscle, immunological and cell proliferations.
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                                neuromuscular disorders, metabolic, endocrine and toxic myopathies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCYTE GENOMICS INC
               paralysis, mental disorders including mood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder; autoimmune thyroiditis; rheumatoid arthritis;
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2000US-224456P.

2000US-226410P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis, Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma; and muscle disorders include cardiac myopathy, myocarditis, polymyositis, arrhythmias and hypertension. The TRICH polynucleotides are used in gene therapy. The present sequence is human TRICH-22 chua
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GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu
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GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu
                           AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG
                                                                                                                                                                                                                                                                                     AsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnVal
                                                                                                       ProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGlu
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RESULT 3
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                                         Prepn. of N-terminal extracellular site protein E.coli transformed by a plasmid comprising the t
  The sequence beta-subunit.
                      Claim 1; Page 2; 12pp; Japanese
                                     binding
                                                                                               05-OCT-1990;
                                                                                                             05-OCT-1990;
                                                                                                                            19-MAY-1992
                                                                                                                                         JP04144683-A
                                                                                                                                                                      Expression
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                                                                                                                                                                      plasmid;
given is the gamma-aminobutyric acid.
This sequence is used in an express
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            GluValLysPheHisLeuGluArgGln
                                                   GAAGAGAAGGATCTGAGATACTGCACCAAGCACTACAACACAGGTAAAATTCACCTGCATT
                                                                 AspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIle
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984.50
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                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                   Alignment
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                                                                                                                                                                                                                                                              Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
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               LeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProPro
                                          CAGTCACCCGAGGACCTGGCCCGTGTGCCCCCCCAACTCCCACCAGCAATATCTTGAACAGG
                                                                                                                                                     ATCTCCTTTTTTATTTTAATGTCCTTG------
                                                                                                                         LysGluGluValLysSerGlyThrLysGlySerGln-----
                                                                                                                                                                             LeuSerPheLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAlaLeuAla 28
                                                                                              AAAGAAAAGTCTTCCAAGAAAGGGAAAGGGGAAAAAGAAGCAGTACTTGTGCCCCATCTCAG
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| US-10-075-846-4 (1-431) | | | ent Similarity: Local Similarity: | | Alignment Scores: | Sequence 39796 | related to ataxia. | disorders related gene therapy, and | The present see protein and po | Claim 6; Page | Novel nucleic act compounds useful gene | WPI; 2000-656166/63. | Rappold-Hoerbrand G; | (RAPP/) RAPPOL | 26-MAR-1999; | 23-MAR-2000; 2 | 05-OCT-2000. | WO200058461-A1 | | exon | intron | exon . | intron | exon | intron | exon | intron | exon | intron | exon | intron | Key exon | Homo sapiens. | Human; ataxia; | Nucleotide sequ |
| × | . 21 | | v: 23.81% | 1.03e 761.0 | | BP; 10630 | | ed to ata: | sequence represents polynucleotides are | 22-44; 47pp; | cid seque | 6/63. | nd G; | RAPPOLD-HOERBRAND G | 99EP-0106343 | 2000WO-EP02600 | | | | . ". | . " | | /*tag= 341963 | | | | | | /*tag= (| | /*tag= 299223 | Location, 298502 | | gene therapy; | sequence of ti |
| AAC61681 (1-3 | | | | 51 | | A; 9337 | defect invo | | | p; English. | acid sequence encoding human ataxia ul for treating disorders relating (| | | D G. | 343. | 600. | | | Ħ | 38996 | k 38781 | .35901 | i 35759 | h 34195 | 9 34114 | 33975 | .33751 | d 33514 | .33444 | 33155 | .33025 | Location/Qualifiers 2985029921 | | apy; ss. | the human a |
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| | • | | | 8 | | 0 other; | ers and di | ne sequences are useful in reagents for identifying and | e. The ata Jand trea | | n protein for to mutations | | | | | | | | | | | | | | | • | | | | | | | | | |
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| GTGGGAGGA | | | PACCEGETEE | | CACGGACAAC | :ThrAspAsn | ratctggaag | rIleTrpLys | CTGTCCTAC | JLeuSerTyr | rgcacccTcc | CTGCCCCTA | | rccagtgaaa | | GAGCCCACC | | CAAGACCACA | rValThrLysThrThrMet- | TCAGGCCCA | GlyPro | STTCTGGAAG | | SCCTGTGTAT | 1 | CCAGGGCTG | | TTGGCAGCA | | CGGCCCAATT | ArgIleArgProAsnPhe-Lys | receerers | SerProSerA | CCAGGGTGG | LeuArgValA |
| CTGAGGGTGGGAGGGTTCCCTTGCACTGTGATGGGCCCCAGTAAGCCGATGTCACT | | 1 | CAGGTGCACCGGGTGGATAGCCAGGAGAGTTTGCGTTAAGGGGGAAGAATTTGGATGAAGA | | GGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCAT | uValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIl | GGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGA | uAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGl | CGAGAATAT | pProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLe | | GGCCCTCCTGCCCCTACAGGCTTGCTGGGCCCCTGGGAATGGCAATGTTTCTGAAGGGCC | | TCCTTCTCCAGTGAAAAATGCCTACTGCCCCTGAGATGTGTTCCCCAACATTCCTCCTCAT | | GTGGGAGGAGCCCACCAGATAACAAGCTGGCATCTTTTGCCATATCAGCCCAAGGAAGG | | CATCACCAAGACCACAAT-GGTAAGGGATCTCCCTGCTCCCCACTTCCAGCCTAGTGTGA | Met | GCTACCCTCAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCATCAGGTTTCAGCTC | GlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSe | GAAGGAGTTCTGGAAGCTGCTCCCAGCCTCCTGGAATGCCCTGCCAATGGCCTGTGCTTT | | CCATGGGCCTGTGTATCTGGCACTGATTTCTCCCAGCAGTGCCCTGGCCTGCAGCTCAGG | | TGGAGGTCCAGGGCTGGGTTCTAACAGCTCAGAAGGAGCCTCCTCACCCCATTGT | . ! | ACCACCTTTGGCAGCACACTAGCCAGCCAGCCCTATTGCCTTCCCTAAGGAAAGGAGGC | 1 | AGGATTCGGCCCAATTTTAAAGGTAAGAAATCTTCATCCTATAAAAACTCCTCCCTC | he-Lys | CCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCC | ProMetSerProSerAspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAla | CTCCTGTCCAGGGTGGCCTTGGCAAAAGAGGGAAGTCAAATCTGGAACCAAGGGGTCCCAG | laLeuAlaL |
| FGCACTGTGA | | | AGAGTTTGCG | | CGCATCTTCA | \rgIlePheL | TCTTTGCTA | PhePheAlaA | CTGATGACT | roAspAspS | ArgValAsnV GGGTGAATG | regeccccre | | reccctgae | | SCTGGCATCT | | GATCTCCCT | | STGACCTGCA | /alThrCysA | SCCTCCTGGA | | ATTTCTCCCA | | CTAACAGCTC | .1 | SCCAGCCCCT | 1 | AGAAATCTTC | | CAAACTTAT | spLysLeuMe | AAGAGGAAGT | /sGluGluVa |
| TGGGCCCCA | | | TTAAGGGGA | 1 | AGAATGGGA | ysAsnGlyA | ATGAGAAAG | snGluLysG | CTCTGGACC | erLeuAspL | alPheLeuA TCTTCTTGC | GGAATGGCA | 1 | ATGTGTTCC | | TTTGCCATA | | GCTCCCCAC | | ACATCTTCA | snIlePheI | ATGCCCTGC | | GCAGTGCCC | | :AGAAGGAGC | 1 | ATTGCCTTC | 1 | ATCCTATAA | 1 | 'GGGGCGAAC | tGlyArgTh | CAAATCTGG | lLysSerGl |
| GTAAGCCGA: | | | AGAATTTGG/ | | ATGTGCTGT | snValLeuT | GGGCCAACT | lyAlaAsnPl | TCGATCCCT | euAspProSe | rgGlnGlnT) GGCAACAGTO | ATGTTTCTG/ | 1 | CAACATTCC | | TCAGCCCAA | | TTCCAGCCT | | TCAACAGTT | leAsnSerP | CAATGGCCT | | TGGCCTGCA | | CTCCTCACC | | CCTAAGGAA | * | AAACTCCTC | | ATCTGGATA | rSerGlyTy: | AACCAAGGG | yThrLysGl: |
| | | 164 | | 164 | | | | neHisGl 144 | | erMetLe 124 | | AAGGGCC 337 | 90 | | 90 | | 90 | | 90 | | neSerSe 84 | | · 67 | | 67 | | 67 | | | | | | rAspAla 60 | | ySerGln 40 |
| 34093 | 5 | | 34033 | 4 | 33973 | 4 | 33913 | 4 | 33853 | 4 | 104 33793 | 733 | | 33673 | | 33613 | | 33553 | | 33494 | | 33434 | | 33374 | | 33314 | | 33254 | | 33194 | | 33134 | | 33074 | |

| 192 192 | | 35054 GAAGCGACTTACCCAAAGTCACAGAGCTACTCTGGGTCAAGGCCCCAACACTGGATGTCTG 35113 | 192 192 | 34994 TTCATGGCAACGCTGAATAGTGGGGAGAGCAGCTACTATAATTCCCCATTTTACAGAAGGG 35053 | 192 192 | 34934 CTATGTGGTCAGCTCTTTAGAGTTCTTAAACCACTTTCACATCCAGGCTCTCAATATCCC 34993 | 192 192 | | 34814 CCTCCTCATCTCCTGGGTCAGGAGACTGTTAGATCTGGAGCCATCCACTAGATGTTCA 348/3 | | 34754 GCTGCCCAAAGTGCAGAGGAACCAAGGATGACAAGGTTGGGTCATCACTTATTTCCACTC 34813 | 192 | 192 | CCACAAACATAGATAACCTTTGTAGAGAGGTAGGAGATGACAGTTCTAGGCACAAGACAG | | 34574 AAGATGCCTATAAAAATGCCAGAGTGGGCAGGGTGGGGGCACTCGTGGAGCCCCTGATTCC 34633 | 192 192 | 34514 TGTCCCCTCTCACAGTGCCTGAAGTAGTTCCACCTTTACCTCTCTGAATTAAGACATTG 34573 | | CAAATGTGTTTTGTGCTGTTTTGGGGGGCGATTTGAGCGACATCTTCTCTGCCCAAACGTA | 192 | 194 VE | GATGAGACTAGAAACCAGGGGTCCCTAACCCCCTAGCCCCAGTGTGTTTTTCATCCCCACG | 192 | AAAAGGCCACTCAGAGTTGGGAAGTTACTCAAGCACACCCAGCCAATTCTTGGCAC | ************************************** | GAGILAKAGAGAGELI ISBAATAAKAGELAGITTAAKELEGAKETICATGAKATCAKAGKAGG | 17.7. OCKORODEKO OKOOKOORKOORKOORKOOKOOKOOKOOKOOKOOKOOKOO | 00100000000000000000000000000000000000 | 178 snPheProMetAspIleGlnThrCysThrMetGlnLeuGluSer 192 | 161116114616166666666666666666666666666 | |
|--|--|---|------------------------------------|--|--|--|--------------|--|--|-------------------------------|--|-----|---|---|---|--|--|---|-----|---|------------|--|---|---|--|---|--|---|--|--|---|--|
| FT /product= "k. sanguineus GlüCli protein, "52" FT /note= "This region is specifically referred in claim 19" XX | CDS 6172377 CDS 6172377 /*tag= a | Kov Printer of | XX OS Rhipicephalus sanguineus. | KW Brown dog tick; glutamate-gated chloride channel; GluCl1; KW GluCl2; crop protection; insecticide; nematocide; acaricide; KW clone T32; ss. | k. sanguineus giucamate-gared chioride channei i c | 28-JAN-2002 (first entry) | AC AAD21397; | AAD21397 ID AAD21397 standard; cDNA; 2400 BP. | RESULT 6 | Db 35894 ACAACACAGGTAAA 35907 | מבן בייייישרייטן יייי מבן. | 231 | Db 35774 TGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGC 35833 | Qy 211 ettysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAlaGluGlyL 231 | ACCCAGCATCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCA | 1019-4 ACCCCAMACLITACICCITOTICACIONOTORIA TO TOTACACO TAMBORIA TOTACACO TOTACACO TOTACACO TAMBORIA TOTACACO TOTACACO TAMBORIA TAMBORIA TOTACACO TAMBORIA TAM | こうしょうせん はんしんしゅん ひまんしゅん ひゅうしゅうしゅうしゅうしゅうしゅう というしょう なまい こうしゅうしゅう ひょうしゅうしゅうしゅうしゅうしゅうしゅう ロー・コント | 35594 A | 192 | Db 35534 AGGAGAGGAGTCTGTAATCTTCCTGATTTACCTGCCCACTCAGGATGGGCCCATGAGACA 35593 | Oy 192 192 | Db 35474 GCTTTCTAGGTCTGTCAGAATAATTTCTCTTTTGGGCTTTTCTCAAGCTTGAGAACAGGGT 35533 | Qy 192 192 | Db 35414 TGAGATATGGCAGGAGGCTCCCAGCTGTGTTCCTTGACATCTTTCCAACCCTCTTGACCT 35473 | Оу 192 192 | Db 35354 GCTCTGAGGCTAGCTCAGCTTAAGACATGTGTTCGGTACACATGCTTACTCCCCTCGGCT 35413 | Qy 192 192 | Db 35294 GCATGACTGGCAGGATATAAATAGCTGTCTCCTCCCTGAGGTGATGTGGCAGAAGTCCTG 35353 | Qy 192 | Db 35234 CTTTAAATTTGCCCCCAACTCAAGGCCCTGGCTAGGATCTATGGTATGCACATTGTCCCAT 35293 | Qy 192 192 | |

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to Rhipicephalus sanguineus (brown dog tick)
-glutamate-gated chloride channel proteins (GluCl1 and GluCl2)
and nucleic acid molecules encoding such proteins. GluCl channel
proteins are useful for identifying modulators. The compounds
identified as modulators are useful for insecticidal, mitacidal
and/or nematocidal treatment for use in animal and human health
and/or crop protection. The compounds are also useful in screening
for and selecting compounds active against parasitic invertebrate
species relevant to animal and human health, including worms,
fleas, ticks, mites and lice. Heterologous cell lines expressing
functional GluCl1 and GluCl2 channel functional forms are useful
for establishing functional or binding assays to identify novel
GluCl1 channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2400 BP;
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              AACATCTTTGTAAGAAGTATCGGCAGAATTGATGACGTCACCATGGAGTACACAGTGCAA
                                 AsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgValAsn
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                                                                             TGCAGGATCCGGCCCATGGGAATTAACAACACAGACGGGCCGGCTCTT---GTACGCGTT
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                               standard; cDNA; 4621 BP
                                                                                                                                                        GTGAGCTCCGGC----
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                                                                                                                        TyrSer-----ProGlnProProAlaPro
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                                                                                                                                                                                                                                            The invention relates to nucleic acid encoding lepidopteran glutamate-gated chloride channels. Glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific-binding or functional assays for identifying potential insecticides. The present sequence is HEGEZ clone cDNA encoding full insections.
                                                                                                                                                                                                           Sequence 4621
                                                                                                                                                                                                                                                                                                                                                                    Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-2000; 2000US-0592891
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LeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro---
                          GAATGCATGAACGGTGGGAAGATCAACTTTCGAGAGAAGGAGAAGCAGATCCTGGATCAG
                                                 GluValLysSerGlyThrLysGlySerGlnProMetSerProSerAspPheLeuAspLys
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chloride channel"
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for insecticidal activity -
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(pos:1125..1127, aa:R)
(pos:1128..1130, aa:F)
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            GluGlySerGlyIleTyrSerProGlnProProAla
                                   CACAGATAGCAACACCACCTTTGCTATGAAACCCTTTGGTGCGCGGCGGCGGCGTGGTGGAATC
                                                                                                                                        CTACTAGAGTTCGCGCTCGTCAACTATGCGTCTCGCTCTGACATGCACCGAGAGAACATG
                                                                                                                                                                LeuLeuGluTyrAlaAlaIleAsnPheValSerArg-----GlnHisLysGluPheIle
                                                                                                                                                                                           TCCTACACGAAAGCCATTGACGTCTGGACTGGTGTATGTCTCACATTCGTATTCGGAGCG
                                                                                                                                                                                                          SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla
                                                                                                                                                                                                                                             ThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysVal
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                                                           PheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMet 404
                                                                                                               ArgLeuArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGlnGluSerArg
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                                                                                      AAGAAAGCGAGACGGGAGATGGAAGCAGCCAGCATGGATGC-TGCCTCAGATCTCCTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
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HEG3E(4)-2 plasmid; cyclic; circular; ds.
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                                                   GluValLysSerGlyThrLysGlySerGlnProMetSerProSerAspPheLeuAspLys
LeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro-
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for insecticidal activity
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Best Local Similarity:
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                                                                                                                                                                                                                                                         Percent Similarity:
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LGIC/GluCl DNA is useful for identifying a compound that modulates glutamate-gated channel protein activity and for identifying a modulator of LGIC/GluCl DNA is useful for identifying a compounds with insecticide screens, validate potential lead compounds with insecticidal activity for use in treating parasitic infections in humans or animals, as hybridisation probes to isolate related genes from other organisms to establish additional pesticide drug screens and also used in competition binding experiments or for functional chloride channel assays to screen for compounds that activate, block or modulate the channel. Heterologous expression of LGIC/GluCl protein allows the pharmacological analysis of compounds active against parasitic invertebrate species values of the content of the channel and the channel and the content of the channel and the channel analysis of compounds active against parasitic invertebrate species.
                                                                                                                                                                                                                                                                                                                                                                                                                                        invertebrate species relevant to animal and human health, especially in the treatment of tick infestations directly related to Dv. LGIC/GluCl protein acts as targets to identify modulators of the channels, where the modulators act as effective insecticidal, acaricidal, mitacidal and/or nematocidal treatments for use in animal and human health and/or crop protection. The modulators are useful for treatment or diagnosis of specific disorders. The present sequence is Rhipicephalus sanguineus in the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel purified nucleic acid molecule encoding Dermancentor variabilis ligand gated ion channel/L-glutamate gated chloride channel protein, useful for identifying modulator compounds that are useful as
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                                                                                                                                                                     GACCACCTGGAGGACGGCGCCACCACGTTCGCCATGAGGCCGCTGGTGCAC
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                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                               The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Rhipicephalus sanguineus GluCl DNA probe which is used for cloning Dermacentor variabilis GABA-gated chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic; GABA-gated chloride channel; recombinant expression; domestic animal;
                                                                                                                                                                                                                                                                    No . .
                                                                                                                                                                                                                                                                                                    Sequence 1197
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                               AspProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMet
                                                      AGAATTGATGACGTCACCATGGAGTACACAGTGCAAATGACGTTCAGAGAGCAGTGGCGG
                                                                            SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn
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                                                                                                                                                        standard;
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Location/Qualifiers
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Brown dog tick; glutamate-gated chloride channel; GluCl2; crop protection; insecticide; nematocide; clone Tl2; ss.
                                                                                        R. sanguineus glutamate-gated chloride channel 1
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L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2)
and nucleic acid molecules encoding such proteins. GluCl channel
proteins are useful for identifying modulators. The compounds
identified as modulators are useful for insecticidal, mitacidal
and/or nematocidal treatment for use in animal and human health
and/or crop protection. The compounds are also useful in screening
for and selecting compounds active against parasitic invertebrate
species relevant to animal and human health, including worms,
fleas, ticks, mites and lice. Heterologous cell lines expressing
functional GluCl1 and GluCl2 channel functional forms are useful
for establishing functional or binding assays to identify novel
GluCl1 channel modulators. The present sequence is R. sanguineus
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             LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 143
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                                                                                                                                                        Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic;
GABA-gated chloride channel; recombinant expression; domestic animal;
                                                                                                                                                                                                                                                                                           AAD22072 standard; DNA; 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeu---ArgAspGluLys 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeu 203
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                                                                                                                                                                                                                                                                                                                                                    GACCACCTGGAGGACGGCGCCACCACGTTCGCCATGAGGCCGCTGGTGCAC
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                                                       "GABA-gated chloride channel protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 5 GABA-gated chloride channel DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide useful for preventing or treating tick infestation, in humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric acid (GABA)-gated chloride channel -
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                                                                                                                                                                                                                                                                                                          ThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThr
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               MetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSer 193
                                                                                                                PheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArg
                                                                                                                                             CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                                                                                                                                                               GACTTCTATTTCCGGCAATCGTGGCGGGACGACGCCACTCTCCAGAAAAGCCCAGAC
                                                                                                                                                                                                                                              GTCACTATGCAGATTATCAGCATAAGTACAGTCTCTGAAGTACAAATGGACTTTACTTCT 273
                                                                                                                                                                                                                                                                    CysAsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgVal
                                             TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
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                                                                      IlePheLysAsnGlyAsnValLeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are usefu as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acid sare also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 8 GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1614
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                                             ATCGGCTCCGGAGGAGAGTTTTCCGCAGTATTCGACTGACGGTGACTGCCAGCTGCCCA
                                                                                                       TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
                                                                                                                      PheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArg
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                                                                                                                                                                                                                                                                                               CCAAGGACAACCGAGGGAAGCACCACCAACCGGATTTAC 1241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGCCGCGGTAGGATATCTCGGCAAG-----AGAATCACCATGAGGAAAACCCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIleThrThrVal
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                                                                                                                                                                                                                                                                                                                         ProLeuLeuArgGluGlyGluThrThrArgLysLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                   GlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSerProGlnProProAla 416
                                                                                                                                                                                                                                                                                                                                                                                                                TTCTTCCAACGAGCCAAGCTCTGAGCCCTTGCTAGCCAGTCCTGAAGTATCCATTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TyrAlaAlaIleAsnPheValSerArgGlnHisLysGluPheIleArgLeuArgArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAGTATCGACGTCTACCTGGGCACATGTTTCGTAATGGTGTTTACCGCGCTCCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCACGATGACCACACTCATGTCCAGTACCAACGCAGCGCTGCCCAAAATATCCTACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTTTTGGCTCCACCGTGACGCTAGTCCAGCTCGCGTCGCGCCTCGGCGTCACCACCGTG
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                                                                                                    obutyric acid; GABA; tick chloride channel; recombi
                                                                          variabilis
                                                                                                                                                                             (first entry)
                            Location/Qualifiers
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                                                                                                                                                                                                                                       DNA; 1614
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 "GABA-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GlyLeuGly-----
                                                                                                       recombinant
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                                                                                                                                                GABA-gated chloride channel
                                                                                                                   infestation;
                                                                                                     expression;
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                                                                                                                   mite;
                                                                                                       domestic
                                                                                                     antiparasitic;
omestic animal;
protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HisCysLeu
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                                                                                                                                                                                                                                                                                                                                                   US-10-075-846-4 (1-431) x AAD22071 (1-1614)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase Chain Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide useful for preventing or treating tick infestation, in humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1614 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chloride channel DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng Y, Cully D,
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               PheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArg
                                                                                                                CTCGAGAGCATGACTGTGGGCGCTGAAGTGGCCGAGAGGATCTGGGTACCCGACACCTTC
                                                                                                                                  ---AspSerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhe
                                                                                                                                                                         GACTTCTATTTCCGGCAATCGTGGCGGGACGAGCGACTCTCGTTCCAGAAAAGCCCCAGAC
                                                                                                                                                                                                                                                CysAsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgVal
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ATCGGCTCCGGAGGAGAGGTTTTCCGCAGTATTCGACTGACGGTGACTGCCAGCTGCCCA
                                                         TTCGCCAACGAGAAGAGCGCCTACTTTCATGCGGCCACAACGCCCAACACTTTCCTCCGC
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| ProproAlaproLeuleuargGluGIyGLUThrThrargLysLeuTyr 429GGCATCCCAAGGACAACCGAAGCAACCAACCGGATTTAC 1241 | HisCysLeuGlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSerProGln 413 | CAA | <pre>IleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGly 393</pre> | | ArgGlnArgArgGlnArgLeuGluGluAspIle 379 | TACGCCGCGGTAGGATATCTCGGCAAGAGAATCACCATGAGGAAAACC 1044 | TyrAlaAlaIleAsnPheValSerArgGlnHisLysGluPheIleArgLeuArgArg368 | AAGAGTATCGACGTCTACCTGGGCACATGTTTCGTAATGGTGTTTACCGCGCTCCTGGAG 996 | LysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAlaLeuLeuGlu 349 | CTCACGATGACCACACTCATGTCCAGTACCAACGCAGCGCTGCCCAAAATATCCTACGTC 936 | LeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysValSerTyrVal 329 | TCCTTTTGGCTCCACCGTAACGCTAGTCCAGCTCGCGTCGCGCTCGGCGTCACCACCGTG 876 | SerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIleThrThrVal 309 | GGCTACTACCTGATCCAGATCTACATCCCGGCCGGATTGATCGTGGTTATTTCCTGGGTC 816 | GlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleValIleLeuSerTrpVal 289 | AACTACTCCCGCCTGGTATGTGAAATACGGTTCGCCCGCTCCATG 756 | HisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGluArgGlnMet 269 | CCGCAGTTCAAGGTCCTCGGTCACGTCCAAAAAGCCAAAGAGGTTGCCCTAACGACAGGA 711 | IleLeuArgAspGlu | ATCCGCTACCGGTGGTCGGACGGTGACACGTCCGTCCGCAAGGAGGTAGAGTTG 651 | LeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeu 233 | AGCTTTGGTTATACCATGAAAGAC 591 | SerIleLeuCysSerProLeuProSerLeuSerLeuSerValGlyTyrThrMetLysAsp 213 | ATGGATCTCAGATACTTCCCGATGGACAGACAAGCGTGCACTATAGAGATAGAA 567 | MetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSer 193 |

Search completed: June 30, 2003, 23:13:41 Job time: 383.186 secs

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Result
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-DB=ISSUEd_Patents_Na -QPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10075846_@CGN 1_1_84_@runat_25062003_163649_5167 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARM_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL-frame+_p2n.model -DEV-xlp
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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| 529. | | 603. | 603. | 610. | 61 | 619. | 625. | 625. | 62 | 64 | 65 | 65 | 65 | 65 | 66 | 66 | 670. | 670. | .67 | 67 | 680. | 680. | 683. | 683. | 687. | 687. | 687. | 71 | 71 | 71 | 71 | 720 |
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| 669 | 2310 | 1652 | 1652 | 1638 | 2191 | 1707 | 1650 | 1650 | 2635 | 1732 | 2508 | 2508 | 2544 | 2544 | 2601 | 2601 | 1542 | 1542 | 1479 | 1479 | 1555 | 1297 | 1917 | 1917 | 2059 | 1970 | 1970 | 1866 | 1491 | 1491 | 2066 | 2066 |
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| us-09-002 ₋ 361-7 | -08-417-330A | -09-436-063C- | US-09-627-650B-2 | -417-330A- | US-08-417-330A-11 | -08-809-8 | PCT-US94-09589-1 | -08-459-1 | -08-768-3 | -08-417- | -09-436-C | -09-627-650B- | -09-43 | -09-62 | -063C-1 | 9-62 | -US95 | 8-24 | ū | US-08-249-112-2 | -08-809-802- | -09-130-3 | -09-436-063C- | 09-627 | -US92-08558- | T-US92-08558- | US-08-072-064-9 | w | 8-768-30 | -08-137-614A | 8-072- | 4- |
| e 7, App | e 15, Ap | e 2, 1 | e 2, 1 | Sequence 13, Appl | e 11, | e 7, App | Sequence 1, Appli | e 1, | e 3, 7 | e 17, | Sequence 8, Appli | e 8, | @ 4 | e 4, A | e 10, | e 10, | 1 | ۲, | Ņ | Ø | e 11, | ο ω, | e 6, | e 6, | e 2, | e ω, | e 9, 1 | e 19, | e 1, | æ | ი ა | Sequence 3, Appli |

ALIGNMENTS

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LENGTH: 4621
TYPE: DNA
ORGANISM: Heliothis virescens
FEATURE:
NAME/KEY: unsure
LOCATION: (764)...(764)
OTHER INFORMATION: n is a, t, g
US-09-592-891A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-592-891A-13; Sequence 13, Application; Patent No. 6329174
    Best Local Similarity:
                      Percent Similarity:
                                            score:
                                                                               Alignment Scores:
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SOFTWARE: FastSEQ for
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
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    PheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMet ::: ::: ||| ||| |||||
                                                                                                                                                                     LeuLeuGluTyrAlaAlaIleAsnPheValSerArg-----GlnHisLysGluPheIle
                                                                                                                                                                                                                                                                                                          SerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu---GlyCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCACAATGGAATACTCCGTACAGTTAACGTTTCGGGAACAATGGTTAGATGAACGGCTC
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                                                               AAGAAAGCGAGACGGGAGATGGAAGCAGCCAGCATGGATGC-TGCCTCAGATCTCCTAGA
                                                                                           ArgLeuArgArgGlnArgArgGlnArgLeuGluAspIleIleGlnGluSerArg
                                                                                                                                                CTACTAGAGTTCGCGCTCGACTATGCGTCTCGCTCTGACATGCACCGAGAGAACATG
                                                                                                                                                                                                                                TCCTACACGAAAGCCATTGACGTCTGGACTGGTGTATGTCTCACATTCGTATTCGGAGCG
                                                                                                                                                                                                                                                       SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla
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Best Local Similarity:
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SOFTWARE: FastSEQ for
SEQ ID NO 11
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APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
TILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                          CCGAACGTGTACATCCGAATCTTCCCCAACGGCAACGTGCTGTACAGCATCCGAATCTCC
                                                                                                                                                                                                                                TrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThr 147
                                                                                                                                                                                                                                                                                                                                                                        GTCACAATGGAATACTCCGTACAATTAACGTTTCGGGAACAATGGTTAGATGAACGGCTC
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                                          CTGACGCTCTCGTGCCCCATGAACCTCAAGTTGTACCCCCTGGATAAGCAGACCTGCTCG
                                                               LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr 187
                                                                                                                                                TGGATGCCTGATCTTCTTCTCCAACGAGGAAGGTCATTTCCACAACATCATCATG
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  MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal
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| RESULT 3 US-09-130-339-1 Sequence 1, Application US/09130339 Patent No. 6358701 GENERAL INFORMATION: APPLICANT: Cully, Doris F. APPLICANT: Cully, Doris F. APPLICANT: Cohen, Charles J. APPLICANT: Etter, Adrian APPLICANT: Cohen, Charles J. APPLICANT: Brochu, Richard M. APPLICANT: Brochu, Richard M. APPLICANT: Brochu, Richard M. APPLICANT: DIVENTION: DNA MOLECULES ENCODING CTENOCEPHALIDES TITLE OF INVENTION: DNA MOLECULES ENCODING CTENOCEPHALIDES TITLE OF INVENTION: DNA MOLECULES ENCODING CTENOCEPHALIDES TITLE OF INVENTION: DNA MOLECULES ENCOPING CTENOCEPHALIDES TITLE OF | Db 688 CTCAGGATG |
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                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             Score:
                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE

COMPUTER SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, VE

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: US/08/435,933

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, III John W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 19264

TELEPHONE: (908) 594-3905

TELEPHONE: (908) 594-3905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (908) 594-472 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                           ArgPro----AsnPheLysGlyProProValAsnValThrCysAsnIlePheIle 79
                                                                                    AAGGAGAAAAAAGTCTTAGATCAAATTTTAGGT----GCAGGCAAATACGACGCCCGAATA
                                                                                                             SerProSerAspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIle 62
                                                                                                                                                                                                                        ACCCCCATTCCCAACATGGGCAGCGGACACTATTTCTGGGCG-----
                    TACTTTGCCAGCCTGTGCAGTGCTTCACTAGCAAATAATGCCAAGGTAAATTTCCGAGAA
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Arena, Joseph P.
Paress, Philip S.
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APPLICANT: Paress, APPLICANT: Liu, Ker TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                     GTGTCTGACGTTCGTGTTCGGGGCCCTGCTCGAGTTCGCCCTGGTGAACTATGCATCCCG 1402
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                                                                                                                                                                                                                                      ATCAGGTTCGAATAAAGCTAACATGCATAAGGAGAATATGAAAAAGAAGCGCCGCGATCT 1462
                               Cully, Doris F.
Arena, Joseph P.
Paress, Philip S.
               Ken K.
                                                                                                                                                                                                     373
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DNA ENCODING GLUTAMATE GATED CHLORIDE
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Percent Similarity:
Best Local Similari
Query Match:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 1
MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 19264 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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NAME: Glesser, Jody M.
REGISTRATION NUMBER: 32,
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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О.:
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CLASSIFICATION:
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                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 12
LENGTH: 1640
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09592891A Patent No. 6329174
                                                                                                                                                     APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
                                                   ORGANISM: Artificial Sequence
                                                                       TYPE: DNA
                                    FEATURE:
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                                                                                                                         FastSEQ for Windows Version
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Best Local Similarity:
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                                 GTGACGACTTTACTTACAATGGCGACCCAGTCGTCAGGCATCAACGCGTCCCTACCACCG
                                                    GTGTCCTGGGTGTCCTTCTGGCTGGACCAGGGAGCTGTGCCTGCGAGGGTCTCACTAGGA
                                                                                                             LeuSerTrpValSerPheTrpIieAsnMetAspAlaAlaProAlaArgValGlyLeuGly 305
                                                                                                                                                      AAACGCGAGTTCAGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATC
                                                                                                                                                                        GluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleValIle 285
                                                                                                                                                                                                                    TACTGCAACAGTAAGACTAATACCGGTGAATACAGTTGCCTGAAGGTAGACCTGCTCTTC
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Query Match:
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US-09-002-361-1
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                                                      US-10-075-846-4 (1-431) x US-09-002-361-1 (1-1844)
                                                                                                                             Percent Similarity:
                                                                                                                                              Score
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price
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                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                           NO...
                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                          LeuProGlyGlnValLeuLeuArgValAlaLeuAlaLysGluGluValLysSerGlyThr
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LeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSer 411
                                                    AGATTCACTGCTGTTCAAAAAATGGCCGCCGAGAAGAAAATGCAAATA-------
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                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC Com
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                       No.:
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STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                          LysGlySerGlnProMetSerProSerAspPheLeuAspLysLeuMetGlyArgThrSer
                                                          ATGGCCCTGATTGCACAGGAAACGGGCCACAAACGGATCCATACAGTGCAAGCGGCGACT
                                                                                       ValAlaLeuAlaLysGluGlu-----
                                                                                                                     CTGCCCGCACA---CCGCTGCTAACCATCTGG-----
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                AATCCCAATCCCAATGCAAATGTGGGCGGACCC---GGAGGAGTGGGCCGTTGGACCCGGC 1312
                                                                                             ATCCAAAAGATAGCCGAACAGAAAAAAGCAACAGCTCGACGGAGCGAACCAACAGCAGGCG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/002,361
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MEDIUM TYPE: Diskett
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Best Local Similarity:
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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applicati
Patent No. 5767261
GENERAL INFORMATION:
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APPLICANT: Wolff, Mark
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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CITY: Garden City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                      36 ThrLysGlySerGlnProMetSerProSerAspPheLeuAspLysLeuMetGlyArgThr
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              ValPheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp---
                                                               AsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgValAsn
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                                            AACATGTACGTGCTCTCCATCAGCTCCTTATCTGAAGTGAAAATGGATTTCACCCTGGAT
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US-08-554-659-3; Sequence 3, A
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 Application
                                                              AATGGGGCTCGGGGCCAGCCA--
                                                                                           GlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyrSerProGlnProProAla
                                                                                                                                                                                             ATCCCCCCACCGAGGACCAGCACCCTATCTAGGCCACCACCTAGCCGATTATCGGAGGTT 1277
                                                                                                                                                                                                                                                                                         ArgArg------GlnArgLeuGluGluAsp-----
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                                                                                                                              CGGTTCAAAGTTCACGATCCGAAGGCATATTCTAAAGGCGGTACTTTAGAAAACACTATC 1332
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) .742-4343
TELEPAX: (516) .742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEO ID NO: 3:
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APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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ZIP: 11530-0299
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                                                                                           GTAAGCTACGACAAAAGAGTGAGGCCGAACTATGGAGGACCGCCAGTGGATGTGGGAGTC
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RESULT 12
US-08-072-064-2
; Sequence 2, Application US/08072064
; Patent No. 6008046
; GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Roless
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TOPOLOGY: unl
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CITY: San Francisco
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415/397-8338
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              Sequence 3, Application US/08072064
Patent NO. 6008046
GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICID
 NUMBER
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SEQUENCES:
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DRUG AND PESTICIDE 20
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Query Match:
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REFERENCE/DOCKET NUMBER: OPHD
TELEPHONE: 415/705-8410
TELEPHONE: 415/705-8410
TELEPHONE: 415/397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2066 base pairs
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SOFTWARE: PATEULA:
CURRENT APPLICATION NUMBER: US/(
APPLICATION NUMBER: US/(
TTING DATE: 1930602
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FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
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CITY: San Francisco
STATE: California
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94104
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                                            SerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla 135
                                                                                                    PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp----Asp 115
                                                                                                                                                                                                                                           GlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThrCysAsn
                                                                                                                                                                                   IlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgValAsnVal 96
                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCCCCGCACA---CCGCTGCTAACCATCTGG------CTGGCCATCAAC 178
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              ACACTATCGGTTGGATCAGAGTTCATTAAGAATATTTGGGTACCTGACACCTTTTTTGTA 538
                                                                                  TACTTTCGTCAATTTTGGACCGATCCTCGTTTAGCGTATAGAAAACGACCTGGTGTAGAA 478
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; Sequence 5, Application US/08072064
; Patent No. 6008046
; GENERAL INFORMATION:
APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SC.
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 22
                                                                                                                                                                                   US-08-072-064-5
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San Francisco
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: OF TELECOMMUNICATION INFORMATION: 415/705-8410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2066 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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NUCLEIC ACID
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                                                                                                SerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla 135
                                                                                                                                                                   PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp---Asp 115
                                                                                                                                                                                                                                     GGCGGTGGCAGCATGCTGGGTGACGTAAACATATCCGCTATTCTCGACTCCTTTAGTGTT
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              AATGAAAAACAATCATATTTTCACATTGCAACAACCAGTAATGAATTCATACGTGTGCAT
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SYSTEM: PC-DOS/MS-DOS
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RESULT 15
US-08-137-614A-3
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                                                                                                                                                            STREET: CIII...
STREET: CITY: Rochester
CITY: New York
"TATE: New York
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene Encoding An Insect TITLE OF INVENTION: Gamma-Aminobutyric Acid
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Soderlund, David M. APPLICANT: Knipple, Douglas C. APPLICANT: Henderson, Joseph E
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
    APPLICATION NUMBER:
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Clinton Square, P.O.
                                                                                                                                                                                                                                                                                                                                        Joseph E
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEPAX: (716)263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
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CLASSIFICATION:
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ThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAlaGlu
                                                               LeuGluSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerValGlyTyr
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                                                                                                                                         LeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGln
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Search completed: July 1, 2003, 00:57:28
Job time: 115.6 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlp

-Q-cgn2_1/USPTO_Spool_US10075846/runat_25062003_163649_5181/app_guery.fasta_1.782

-Q-cgn2_1/USPTO_Spool_US10075846/runat_25062003_163649_5181/app_guery.fasta_1.782

-DB-Published_Applications_NA -QFWT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1

-LOOPEXT-0 -LOOPEXT-0 -UNITS-blts -START-1 -END--1 -MATRIX-blosum62

-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100

-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -QUTFWT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0

-MAXLEN-200000000 -USER-US10075846 -GCGN _11_102_erunat_25062003_163649_5181

-NCPU-6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSFBLOCK-100

-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5

-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT 1 US-10-075-846-3

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Sequence 3, Application US/10075846

Publication No. US20030032608A1

GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT FILING D079 NP
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 1640
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1293)
US-10-075-846-3
Alignment Scores:
1.62e-278
Length: 1640
Pred: NO.:
2552.00
Matches:
431
PRIOR FILING APPLICATION NUMBER: US 60/269.535
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                             GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A I
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRA
FILE REFERENCE: DO079 NP
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 2565
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Best Local Similarity:
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A !
TITLE OF INVENTION: IN THE GASTROINTESTINAL TR.
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
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| 68 GlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValThrLys | 51 LeumetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLys | SerGlyThrLysGlySerGl ::: ::: AACGGTGGGAAGATCAACTT | 33.30% Indels: 9 Gaps: 1) x US-09-969-844-13 (1-4621) | No : | OTHER INFORMATION: 09-969-844-13 gnment Scores: | ORGANISM: Heliothis FEATURE: NAME/KEY: unsure LOCATION: (764)(7 | ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 13 ; LENGTH: 4621 ; TYPE: DNA | FILE REFERENCE: A32815-I 072667.0178 CURRENT APPLICATION NUMBER: US/09/969,84 CURRENT FILING DATE: 2001-10-03 NUMBER OF SEQ ID NOS: 14 | ; APPLICANT: Xavier Georges Sarda ; APPLICANT: Michael David Tomalski ; APPLICANT: Vincent Paul Mary Wingate ; TITLE OF INVENTION: Heliothis Glutamate Receptor | ; Sequence 13, Application US/09969844 ; Publication No. US20020192776A1 ; GENERAL INFORMATION: ; APPLICANT: X1ao-Zhou Michelle Wang | RESULT 4 US-09-969-844-13 | 321 AlaSerLeuProLys | Qy 301 ArgValG1yLeuG1yI1eThrThrValLeuThrMetThrThrG1nSerSerG1ySerArg 320 | | Ob 799 GTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGC 858 Qy 281 LeuLeuIleVallleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAla 300 | 261 ValLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrTleProSer 28 | Qy · 241 GluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGlu 260 | QY 221 ASPALAPTOALAVAIGINVALATAGLUGIYLEUTRTLEUPTOGINPHEILELEUATGASP 240 | 634 |
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| RESULT 5 US-09-969-844-11 ; Sequence 11, Application US/09969844 ; Publication No. US20020192776A1 | Qy 405 GluGlySerGlyIleTyrSerProGlnProProAla 416 ::: ::: | Qy 385 PheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGlyGlyProMet 404 | Qy: 365. ArgLeuArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGlnGluSerArg 384 ::: ::: Db 1173 AAGAAAGCGAGACGGGAGATGGAAGCAGCCAGCATGGATGC-TGCCTCAGATCTCCTAGA 1231 | Qy 347 LeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLysGluPheIle 364 | Qy 327 SerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAla 346 | Qy 307 ThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysVal 326 | Qy 287 SerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIle 306 | Qy 267 ArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuILeUIleValIleLeu 286 | Qy 247 CysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGlu 266 | Qy . 228 AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeuGlyCys 246 | Qy 208 GIYTYTThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGinVal 227 | 684 CTCAGGATG | Db 624 TTGACGCTCTCGTGCCCCATGAACCTCAAGTTGTACCCCCCTGGATAAGCAGACCTGCTCG 683 Qy 188 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 207 | 168 LeulleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr | Qy 148 AspAsnLysLeuLeuArgII-BheLysAsnGlyAsnValLeuTyrSetTleArgLeuThr 167 | TGGATGCCTGATCTATTCTTCTCCAACGAGAAGGAAGGTCATTTCCACAACATCATCATG | Db 444 AAATTCAATAATCTTGGAGGTCGCCTCAAATACCTGACACTGACCGAAGCCAACAGAGTC 503 Qy 128 TrpLysproAspLeuphepheAlaAsnGluLysGlyAlaAsnpheHisGluValThrThr 147 | Db 384 GTCACAATGGAATACTCCGTACAGTTAACGTTTCGGGAACAATGGTTAGATGAACGGCTC 443 Qy 108 SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAspSerIle 127 | Qy 88 ThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107 |

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GENERAL INFORMATION:
APPLICANT: XLAO-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Wichael David Tomalski
APPLICANT: Wichael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-1 072667.0178
CURRENT APPLICATION NUMBER: US/09/969,844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 1609
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GTGAAAAACTTACACCTGCCTCGGTTCACGCTG-----GGGAAGTTCCTCACTGACTAC
                                                                                    GlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnVal
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                           AlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu---GlyCys
                                                            CTCAGGATG----
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                   Alignment Scores:
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APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERNACENTOR VARIABILIS
FILE REFERENCE: 20629p
CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/10239420 Publication No. US20030096984A1
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Rhipicephalus
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                                                                                                          7 TTGGACAGCATCATTGGCCAG----GGTCGTTATGACTGCAGGATCCGGCCCATGGGAATT
SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn ::: ||||||||
                                                                                                                            LeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro------
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                                               AACAACACAGAGGGGCGGCTCTT---GTACGCGTTAACATCTTTGTAAGAAGTATCGGC
                                                                           ---AsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer
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RESULT 7

US-09-969-844-12

Sequence 12, Application US/09969844

Publication No. US20020192776A1

Publication No. US20020192776A1

APPLICANT: xiao-zhou Michelle Wang

APPLICANT: Xavier Georges Sarda

APPLICANT: Wichael David Tomalski

APPLICANT: Vincent Paul Mary Wingate

TITLE OF INVENTION: Heliothis Glutamate Rec

TITLE REFERENCE: A32815-I 072667.0178
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                                                                                                                                                                                                                                         AspIleIleGlnGluSerArgPheTyrPheArgGlyTyrGlyLeuGlyHis
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                                                                                                                                                                                                                                                                                                                                   GTATTCGGCGCGCTCCTCGAGTTCGCCCTGGTCAACTACGCCTCGCGGTCAGATTCACGC
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CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: PCR amplified fragment of Heliothis DNA
OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No . :
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                        GluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIleValIle
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                                                                      TACTGCAACAGTAAGACTAATACCGGTGAATACAGTTGCCTGAAGGTAGACCTGCTCTTC
                                                                                        CysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeu
                                                                                                                                                                                             ValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGln
                                                                                                                                                                                                                                                           TCGCTCAGGATG:
                                                                                                                                                                                                                                                                                      ThrMetGlnLeuGluSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer
                                                                                                                                                                                                                                                                                                                    TCCCTGACGCTCTCGTGCCCCATGAACCTCAAGTTGTACCCCCTGGATAAGCAGACCTGC
                                                                                                                                                                                                                                                                                                                                     ThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCys
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                                                                                                                                  GTGGTGAAAAACTTACACCTGCCTCGGTTCACGCTG-
                                                                                                                                                  ValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGluLysAspLeu---Gly
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| | 100 | Ov 24 ArgValAlaLeuAlaLvsGluGluValLvsSerGlvThrLvsGlvserGlnDrnMotSer 43 | Db: 58 CTCCTGGAGCTCCTGCTGCCTGGCTCTCCTGGACCCTG99 | Qy 4 LeuValProAlaThrLeuSerPheLeuLeuLeuTrpThrLeuProGlyGlnValLeuLeu 23 | US-10-075-846-4 (1-431) x US-09-815-925-10 (1-1467) | Indels: Gaps: | Local Similarity: 40.89% Conservative: | 726.50 Matches: | gnment Scores: | US-09-815-925-10 | | FEATURE: | ; TYPE: DNA ; ORGANISM: Homo sapiens | LENGTH: | | PRIOR | | | CURRENT APPLICATION NUMBER: US/09/815,925 | ; TITLE OF INVENTION: Polypeptides ; FILE REFERENCE: 787CIP2H | ; TITLE OF INVENTION: No. US20020127199Alel Nucleic Acids and | APPLICANT: Wehrman, Tom | ; APPLICANT: Yang, Yonghong ; APPLICANT: Zhang, Ite | | | ; GENERAL INFORMATION: : APPLICANT: Tang, Y. Tom | ; Patent No. US20020127199Al | 09-815-925-10 | | Db 1120 ATGAAGAAAGCGAGACGGGAG 1140 | Qy 364 IleArgLeuArgArgGln 370 | Db 1060 GCGCTACTAGAGTTTGCGCTCGACTATGCGTCTCGCTCTGACATGCACCGAGAGAAC 1119 | Qy 346 AlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLysGluPhe 363 | Db 1000 GTGTCCTACACGAAAGCCATTGATGTCTGGACTGGGTTATGTCTCACATTCGTATTCGGA 1059 | Qy 326 ValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheValPheAla 345 | Db 940 GTGACGACTTTACTTACAATGGCGACCCAGTCGTCAGGCATCAACGCGTCCCTACCACCG 999 | Qy 306 IleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLys 325 | Db 880 GTGTCCTGGGTGTCCTTCTGGCTGGACCAGGGAGCTGTGCCTGCGAGGGTCTCACTAGGA 939 | 286 LeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGly | Db 820 AAACGCGAGTTCAGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATC 879 |
|----------|----------------------|---|--|--|---|--|---|--|--|------------------|--|---|--|--|---|-------|---|--|---|--|---|--|---|---|--|--|---|---|---|--|--|--|---|---|---|---|---|---|--|---|
| RESULT 9 | Db | Qy | Db . | Qy | Db | Q Qy | Db | . S |) t | 2 | Qy | Db | Qy | Db | Q.Y | ? | Db | Qy | Db | Qy | Db | . 5 | 2 | Db | Qy | Db | Qy |) 5 | ? | Oy | Db | Qy | Db | Qy | Db | Qy | Db | Qy | Db | Qy |
| | 1090 GCAAAGAATG 1099 | 372 gGlnArgLeu 375 | 1030 TACATTTTCTTTGGAAGAGGCCCTCAAAGGCAGAAGAAGCTTGCAGAAAAGACAGCCAAG 1089 | 355 PheVal-SerArgGlnHisLysGluPheIleArgLeuArgArgArgGlnArgAr 372 | TACCTTATGGGCTGCTTCGTCTTTGTGTTCCTGGCCCCTTCTGGAGTATGCCTTTGTCAAC | TrpMetAlaValCysLeuLeuPheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsn | 910 ATCAACACCCACCTTCGGGAGACCTTGCCCAAAATCCCCCTATGTCAAAGCCATTGACATG 969 | GINSerSerGIySerArgAlaSerLeuProLysValSerTyrValLysAlaIleAspIle | INTERPRETATION OF THE PROPERTY | | 295 MetAspAlaAlaProAlaArgValGlyLeuGlyIleThrThrValLeuThrMetThrThr 314 | 790 CAGACTTATATGCCCTCTATACTGATAACGATTCTGTGGGTGTCCTTCTGGATCAAT 849 | 275 GlnMetTyrIleProSerLeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsn 294 | 730 GCCTATCCTCGACTGTCACTGAGCTTTCGGTTGAAGAGGAACATTGGATACTTCATTCTT 789 | 233 LYSPHETHICYSTIEGIAVAILYSPHEHISDEUGIAKGGIMMEGGIYTYTTYTTEATIE 2/4 | | 673 CAGTTCTCCATCGTGGAGCACCGTCTGGTCTCGAGGAATGTTGTCTTCGCCACACGT 729 | 235 GlnPheIleLeuArgAspGluLysAspLeuGlyCysCysThrLysHisTyrAsnThrGly 254 | ACCGGAGTGGAAAGGATTGAG | 215 ValPheGluTrpLeuGluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuPro 234 | 586 AGCTATGGCTACACCACGGATGACATT 612 | Transfer services the services of the services | T 0 | 535 GACCTCAGGAGATACCCCCTGGACGAGCAGAACTGCACTCTGGAAATTGAA 585 | 175 AspLeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSerSer 194 | 475 CACCCTGATGGGACAGTGCTGTATGGGCTCAGAATCACCACGACAGCAGCATGCAT | 155 PheLysAsnGLyAsnValLeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMet 174 ::: | TIAAATGACAAAAAGTCATITGTGCATGGAGTGACAGTGAAAAAACCGCATGATCCGTCTT | | 135 AlaAsnGluLysGlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArqIle 154 | 355 CTCAACCTCACCCTTGACAATCGAGTGGCTGACCAGCTATGGGTGCCCGACACATATTTC 414 | 115 AspSerLeuAspLeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePhe 134 | 298 ACCATGTATTTTCAACAATATTGGAGAGATAAAAGGCTCGCCTATTCTGGGATCCCT 354 | 95 AsnValPheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrProAsp 114 | 238 ATGAACATCGACATCGCCACCATCGACATGGTTTCCGAAGTCAACATGGATTATACCTTA 297 | 75 CysAsnIlePheIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgVal 94 | 181AAAGGCTACGACATTCGCCTAAGACCCGACTTCGGGGGTCCCCCGGTCTGCGTGGGG 237 | 55 ThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyProProValAsnValThr 74 | 127 GTGAACGATCCCGGGAACATGTCCTTTGTGAAGGAGACGGTGGACAAGCTGTTG 180 | 44 ProSerAsp |

US-10-239-420-3

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CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-075-846-4 (1-431) x US-10-239-420-3 (1-3442)
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Publication No. US20030096984A1
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3442
TYPE: DNA
ORGANISM: Dermacentor variabilis
FEATURE:
                                                                                                                                  416 GAGTTCCAATATGTCACAGTACCTAATGTACTGGTCCGCGTTAACCCCGAACGGAAAGATT
                                                                           LeuTyrSerIleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPhePro
                                                                                                                                                                                                                                                    ProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAla
                                                                                                                                                               AsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnVal
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  MetAspIleGlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeu
                                             CTATACATGCTCAGGCTCAAGCTAAGGTTTGCATGTATGATGGATCTATATCGCTTTCCT
                                                                                                                                                                                                                        CCAAAGCTGGTGCAGCGTATATGGAAACCAGAAGTATTCTTCGCAAATGCAAAACACGCA
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                                           US-10-075-846-4 (1-431) x US-10-239-420-1 (1-3598)
                                                                                                           Query Match:
                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                           Score:
                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                    US-10-239-420-1
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23.
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEO ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 3598
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10239420 Publication No. US20030096984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cully, Doris F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED TO
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                                 FEATURE: NAME/KEY: CDS
LOCATION: (170)...(1363)
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Dermacentor variabilis
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LeuSerPheLeuLeuTrp---
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                                                                                                           Conservative: Mismatches: Indels:
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-ThrLeuProGlyGlnValLeuLeuArg
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Alignment Scores: Pred. No.:

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Query Match:
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NAME/KEY: CDS
LOCATION: (88)..(1512)
US-10-037-270-131
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TITLE OF INVENTION: No. US20030104529A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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SQFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 131
LENGTH: 1693
TYPE: DNA
ORGANISM: Homo sapiens
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Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
Tillinghast, John
ProAsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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                                                                                                                                    SerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn 103
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Wang, Jian-Rui
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Xue, Aidong J.
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Zhang, Jie
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| ; SOFTWARE: PatentIn version 3.0 SEQ ID NO 96 ; LENGTH: 1866 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-964-824a-96 | PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR FILING DATE: 2000-09-28 PRIOR FILING DATE: 2000-09-28 | Patent No. US2002010251A1 Patent No. US2002010251A1 GENERAL INFORMATION: APPLICANY: HOLLIGATION: Stephen TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu TITLE OF INVENTION: Sets FILE REFERENCE: 689290-73 CURRENT APPLICATION NUMBER: US/09/964,824A CURBENT APPLICATION NUMBER: US/09/964,824A | Qy 344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheVal 356 | Db 919 CTAGGAATCACGACGGTGCTTACAATGACAACCATCAGCACCCTCAGGGAGACCCTG 978 Qy 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343 | Oy 284 ValileLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 Oy 284 ValileLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 Db 859 ACAATTCTGTCCTGGGTGTCTTTTGGATCAACTATGATGCATCTGCAGCCAGAGTCGCA 918 Oy 304 LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 | 244 LeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe :::: | Qy 204 SerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaPro 223 | Oy 164 IleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIle 183 ::: ::: ::: ::: 544 CTCCGAATCACAACCACAGCTGCATGTATGATGATGATGTTCGAAGATATCCACTGGATGAG 603 Qy 184 GlnThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeu 203 :::::: 604 CAGAACTGCACCCTGGAGATCGAA | Qy 124 LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 143 |
|--|--|--|--|---|---|--|--|--|---|
| Qy 284 ValIleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 | Qy 244 LeuGLYCYSCYSTDTLYSHLSTYTASTTDGTYLYSPDETDTCYSTLEGLUVALLYSPDE 263 ::: | 204 SerLeuservalGlytyrThimetLysaspheuvalpheGulTrpleuGluAsphlapro | 488 CTCCGAATCACAACCACAGCTGCATGTATGATGGATCTTCGAAGATATCCACTGGATGAG 184 GlnThrCysThrMetGlnLeuGluserSerSerIleLeuCysSerProLeuProSerLeu | Qy 144 GluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSer 163 | Qy 104 ASPECARGLEUSETTYRATGGLTUYRFFOASPASDSETLEUASPEROSETREE 123 | 101 ACCROACT COCCATTOR ACCROACT COCCACATOR ACCACATOR ACCROACT COCCACATOR ACCROACT COCCACATOR ACCACATOR ACC | Db 80 GTGATGATTACCATGGTCTGTTGTGCACACAGCACCAATGAACCCAGCAACATGCCATAC 139 Qy 44 ProSerAspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArg 63 Qy 64 ProAsnPheLysGTGGGACAGATTGCTCAAAGGATATGACATTCGCTTGCGG 190 Qy 64 ProAsnPheLysGTyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer 83 | US-10-075-846-4 (1-431) x US-09-964-824A-96 (1-1866) Qy | Alignment Scores: 2.04e-78 Length: 1866 Score: 694.50 Matches: 144 Percent Similarity: 60.06% Conservative: 68 Best Local Similarity: 40.79% Mismatches: 116 Query Match: 30.84% Indels: 25 DB: 6 |

| ProGlyGlnValLeuLeuAr ::::: | US-10-075-846-4 (1-431) x US-10-211-673-11 (1-1555) | 30.22% Indels: 9 Gaps: | Fred. No.: 9.42e-77 Length: 1555 Score: 680.50 Matches: 161 Percent Similarity: 50.11% Conservative: 63 Best Local Similarity: 36.02% Mismatches: 150 | Scores: | ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-211-673-11 | NAME/KEY: Coding Sequence LOCATION: 471402 OTHER INFORMATION: | STRANDEDNESS: single HOLECULE TYPE: cDNA | ; SEQUENCE CHARACTERISTICS: ; ELENGTH: 1555 base pairs ; TYPE: nucleic acid | INFORMATION FOR SEQ ID NO: 11: | TELEPHONE: 732-594-1307 TELEFAX: 732-594-4720 | REFERENCE/DOCKET NUMBER: 11292 TELECOMMUNICATION INFORMATION: | ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: BEGISTERATION NUMBER: 45 242 | | lg-2002 lnknown> | SUTWARE: FASTSEQ FOR WINDOWS VERSION 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/211.673 | IBM Compatible SYSTEM: Windows | | COUNTRY USA | ; STREET: P.O. Box 2000, 126 E. Lincoln Ave. ; CITY: Rahway . CTATE. NT | ONDENCE ADDRESS: DDRESSEE: Merck & Co., Inc | ITTLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT NUMBER OF SPOTFACES: 14 | (1) | ; PUDIICATION NO. USZUJUJIJISMAI ; GENERAL INFORMATION: | RESULT 13 US-10-211-673-11 : Sequence 11, Application US/10211673 | 983 TTCCTGGCTCTGGAGTATGCCTTTGTAAATTACATC | Qy 344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheVal 356 | Qy 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343 ::: :::::: ::: | Db 863 CTAGGAATCACGACGGTGCTTACAATGACAACCATCAGCACCCTCCAGGGAGACCCTG 922 |
|-----------------------------------|---|---|---|---------|--|--|---|---|--|--|--|---|--------------|---|---|--|--|--|---|---|---|--|---|--|--|--|--|---|
| Qγ | ф | Qy | Фр | ф | Qy | Оy | Db | Ov Db | Qy | Db | Qу | Qy Db | P D | Qy | Db | Qy | da Vy | 2 5 | Qy Sh | Db | Qy | Db | Qy | Qy Db | Db *2 | ov . | Qу | Db |
| 356ValSerArgGlnHisLysGluPhe, | 1022 GTGGAGTACGCCTTTGCTCATTTCAACGCCGACTACAGGAAGGA | 348 LeuGluTyrAlaAlaIleAsnPhe 355 ::: | 328 TyrValLysalalleAspIleTrpMetAlaValCysLeuLeuPheValPheAlaAlaLeu 347 ::: ::: :::: ::: ::: ::: | | ThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeuProLysValSer | 288 TrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGlyLeuGlyIleThr 307 | | 722 ATGAACTTCAAGTCCGCTGGCCAGTTCCCACGGCTCAGCCTGCACTTCCACCTGCGGAGG 781 268 GlnMetGlvTvrTvrLeuIleGlnMetTvrIleProSerLeuIeuIleValIleLeuSer 287 | ThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPheHisLeuGluArg | 662 CTGGACAAGCTGCAGCTGGCGCAGTTCACCATCACCAGCTACCGCTTCACCACGGAGCTG 721 | Ile | 208 G1yTyrThrMetLysAspLeuValPheG1uTrpLeuG1uAspA1aProA1aVa1G1nVa1 227 ::: :: ::: ::: | CTGGACCTGGAG | 188 MetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 207 ::: | | 168 LeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThr 187 | 146 ASPASIDYSLEULEUARGLIEPINELYSASINGIJASINGILEUTYSSETILEARGLEUTIR 16/ ::: - - - - :: - 464 GAGAACAAGCTCATCCGGCTGCAGCCCGACGGGGTGATCCTGTACAGCATCCGAATCACC 523 | TOURIST TOUR CONTROL OF THE ACCURACY CONTROL OF THE AC | TrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluValThrThr | 347 TCCTACAACCACACCAACGAGACCCTGGGCCTGGACAGCCGCTTCGTGGACAAGCTG 403 | ArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAspSerI | GCCAACATGGAGTACACCATGACGGTGTTCCTGCACCAGAGCTGGCGGGACAGCAGGCTC | 88 ThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107 | 68 GlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValThrLys 87 | Trece and the second of the se | | 35 GlyThrLysGlySerGlnProMetSer | 48 TGGACGCG-CCCGCCCGGCTGCTGGCCCCGCTCCTGCTCCTGCGCGCAGCAGCTCCGC 106 |

| Pred. No.: 1.26e-75 Pred. No.: 130 Score: 670.00 Matches: 130 Percent Similarity: 41.148 Mismatches: 91 Ouery Match: 22 DB: DS: 110 AspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgPro 64 111 111 111 112 113 US-10-075-846-4 (1-431) x US-10-239-420-13 (1-1150) Qy 46 AspPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSer 84 111 112 113 Qy 55 AsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSer 84 113 Qy 55 AsgTCACCTCGGAAATGCAACTATTGTGTCATGCGAAATTTACATACA | FILING APPLICA FILING OF SEQ OF FAS RE: Fas RE: Fas RE: I150 | US-10-239-420-13 ; Sequence 13, Application US/10239420 publication No. US20030096984A1 ; GENERAL INFORMATION: APPLICANT: Cully, Doris F. APPLICANT: Zheng, Yingcong TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS FILE REFERENCE: 20629P CURRENT APPLICATION NUMBER: US/10/239,420 ; PRIOR APPLICATION NUMBER: PCT/US01/09956 | TCTGCTGCCGGCGTCACGAGGAGCTGGCCATCTCCC GluGluAspIleIleGlnGluSerArgPheTyrPheJ | 364 |
|--|---|---|--|--|
| WS-10-239-420-4 Sequence 4, Application US/10239420 Publication No. US20030096984A1 GENERAL IMPORMATION: APPLICANT: Cully, Doris F. APPLICANTON: CHANNELS ENCODING LIGAND GATED ION TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS FILE REFERENCE: 20629 CURRENT FILING DATE: 2002-09-23 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR APPLICATION NUMBER: 60/193,935 PRIOR | Qy 304 LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 | Qy 244 LeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe 263 | ### ################################## | Db 371 TATGTGACTGTACCTAACGTCCTCGTTAGGATCAACCCGACTGGAATAATCTTGTACATG 430 Qy164 IleargLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIle 183 |

| Qy 336 pb 1013 | Qy 316 Db 953 | Oy 296 Db 893 | Qy 276 Db 833 | Qy 256 Db 773 | Qy 236 Db 716 | Qy 216 Db 659 | Oy 196 Db 638 | Oy 176 Db 581 | Qy 156 Db 521 | 9 | Oy 117 Db 401 | Qy 97 Db 344 | Qy 77 Db 284 | Oy 58 | Oy 38 Db 174 | Oy 18 Db 123 | US-10-075-846- | Best Local Simila Query Match: DB: |
|--|---|---|--|---|---|---|---|---|--|--|--|---|---|--|---|--|-------------------------|--|
| MetAlaValCysLeuLeuPheV | SerSerGlySerArgAlaSerLeuPr AGCTCCGACCACCAGGCCAACCTAGC | ASPAlaAlaProAlaArgValG | MetTyrIleProSerLeuLeuI ::: TCTTACCTGCCGTCCACACTCA | PheThrCysIleGluValLysPl:::::::::::::::::::::::::::::::::::: | PheIleLeuArgAspGluLysA: ::: ::: TTCGAGCTTCAACAAATCA | PheGluTrpLeuGluAspAlaPı ::: ::: CTCCAATGGGGAAACGCTG/ | LeuCysSerProLeuProSerLe | LeuLysAsnPheProMetAspIleGlnThrCysThrMetGlnLeuGluSerSerSer:::::::::::::::::::::::::::::: | LysasnGlyasnValLeuTyrSerIleargLeuThrLeuIle | AsnGluLysGlyAlaAsnPheH | LeuAspLeuAspProSerMe CTAGACTTAAACGACCCCAACCT | PheLeuArgGlnGlnTrpAsnAspProArgLeuSerTyrArgGluTyrPro ::: | IlePhèIleAsnSerPheSerSerValThrLysThrThrMetAspTyrArgValAsn | TyrAspAlaArgIleArgPro | GlySerGlnProMetSerProSerA GACTCTTCGATGATGTCGACCTT-C | ProGlyGlnValLeuLeuArgValAlaLeuAlaLysG | 4 (1-431) x US-10-239-4 | ilarity: 33.33% 29.09% 9 |
| ysLeuLeuPheValPheAlaAlaLeuLeuGluTyrA ::: ::: GCACCATGTTCGTGTTCGCCGCGGTGCTCGAGTTCA | OLYSVa] GCCGGTC | lyLeuGlyIleThrThr ::: GCTGGGTGTCACCACG | leVallleLeuSerTrp ::::: CGTGGTCGTGTCGTGG | neHisLeuGluArgGln ::: ::: CAACTTGAAGCGTTCC | AspLeuGlyCysCysThr AGCCTGACGAAGTGCAGC | ProAlaValGlnValAla ::: SAGGCTGTCACCATGTAC | uSerLeuSerVal | leGlnThrCysThrMet ::::: saCAGGTCTGCAGCATC | erIleArgLeuThrLeu | lsGluValThrThrAsp arrcgrcactgrtccc | <pre>stLeuAspSerIleTrp :: :: CCTCAAGAAAGTGTGG</pre> | pProArgLeuSerTyr ::: CTTGCGGATGAAGAAC | erValThrLysThrThr | AsnPheLysGlyPro ::: TCATCATTTAAACGTT | eraspPheLeuAspLysLeuMetGly | lAlaLeuAlaLysGluG ::: CACATCGACAAAGGAT- | 20-4 (1-2194) | <pre>Mismatches: Indels: Gaps:</pre> |
| GluTyrAlaAlaIleAsnPhe ::: GAGTTCACCTTCGTCTCCTAC | SerTyrValLysAlaIleAspIleTrp ::: TGGTACGTGAAAGCGCTCGACGTGTGG | AlaProAlaArgValGlyLeuGlyIleThrThrValLeuThrMetThrThrGln ::: ::: ::: ATACCGGCGCATCACGCTGGGTGTCACCACGCTCCTACTATTTCGTCGGAG | TyrIleProSerLeuLeuIleValIleLeuSerTrpValSerPheTrpIleAsnMet :: ::::: | alLysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGln ::: ::: ::: ::: ::: :::GGAGCTCAACTTGAAGCGTTCCATTGGCCACCACCTAGTGCAG | rLysHisTyrAsnThrGlyLys : : : : CGGCGCCTTTCAGATAGGCGAG | aGluGlyLeuThrLeuProGln :: CAGTGGTCTGAAGATGGCACAA | 3lyTyrThrMetLysAspLeuVal ::::: AAGACGACAAAGGAGGTTGAG | GlnLeuGluSerSerSerIle ::: GAGCTTGCCTCATTTTCC | IIleLeuSerCysLeuMetAsp ::: ::: ACATTCTCCTGCATGATGAAC | luLysGlyAlaAsnPheH1sGluValThrThrAspAsnLysLeuLeuArgIlePhe | AspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAla ::::: | ArgGluTyrProAspAspSer GCCAACCTGACCCGGTCC | MetAspTyrArgValAsnVal ATGGACTACGACGTAGACCTG | laargIleargProAsnPheLysGlyProProValAsnValThrCysAsn | LeuMetGlyArgThrSerGly ::::: ATCTTATGGAGC | GluValLysSerGlyThrLys :::ACCCAGCACCAG | | 133 94 14 |
| 1072 | 335 | 315 952 | 295 892 | 275 832 | 255 772 | 235 715 | 215 658 | 195 637 | 175 · 580 | 155 520 | 135 460 | 116 400 | 96 343 . | 76 283 | 57 223 | 37 173 | | |

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| 1429 | 411 | 1372 | 393 | 1312 | 389 | 1252 | 383 | 1192 | 379 | 1132 | 373 | 1073 | 356 |
| CCATCACCGACGCACGCTCTGGTGGAAGAGAAAGCTACA 1467 | SerProGlnProProAlaProLeuLeuArgGluGlyGluThr 424 | 1372 GAAACGGGTGGCTGCCTACCCCAGGGAAACGGTCGGCCGCTGGATTGAAAAGGACTG 1428 | GlyHisCysLeuGlnAlaArgAspGlyGlyProMetGluGlySerGlyIleTyr 410 | 1312 CTAGTTGGCCATGGTCTCAGTGCCTACAGCTGCTGCTCCCAACGTGCAGCCATACGCCGG 1371 | GlyTyrGlyLeu | 1252 GGTCGCTTTCCCCAATCGGCTTTGTTCTCTTCAACGCACTCTACTGGCCCTATTACTTGCT 1311 | Ser, | 1192 GTCCACCCACGTGGTCTTGGCTTACAGACACCGTGCCAAGCAGATCGACCAAGTGAGCCG 1251 | IleIleGlnGlu 382 | 1132 TCTCGTTCTTGTCGTGGGAAACAAGGACAAAAATCGACCCCCGTCACCGTCCATCCCGAC 1191 | GlnArgLeuGluGluAsp 378 | 1073 CTCGCTCGCAGAAA-GCAGATCGTGCCCGCCTCTATCGCGGACGTCGAGGCTTCCCAAGA 1131 | ValSerArgGlnHisLysGluPheIleArgLeuArgArgGlnArgArg 372 |

Search completed: July 1, 2003, 01:01:34 Job time : 248.481 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Command line parameters:

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-MODEL-framet_p2n.model -DEV=xlp
-O-/cgn2_1/USPTO_Spool_VS10075846/runat_25062003_163648_5157/app_query.fasta_1.782
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10075846_6CGN_1_1_3724_@runat_25062003_163648_5157 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MANIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 200000000 Database Total number of hits satisfying chosen parameters: Searched: Scoring table: Title: Perfect score: OM protein - nucleic search, using frame_plus_p2n model 0 : US-10-075-846-4 2252 1 MTTLVPATLSFLLL June 30, 2003, 23:00:29 ; Search time 2265.88 Seconds (without alignments) 3080.588 Million cell updates/sec Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext 16154066 seqs, 8097743376 residues BLOSUM62 MTTLVPATLSFLLLWTLPGQ......PQPPAPLLREGETTRKLYVD em_gss_hum:*
em_gss_inv:*
em_gss_pln:* gb_est1:* em_estro:* em_estov:* em_estmu:* em_estin: * em_esthum: * em_estba:* gb_est2:*
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gb_est3:* em_estpl:* em_gss_rod:* em_gss_mus:* em_gss_mam:* em_gss_fun:* em_gss_vrt:* gb_gss:* em_estom:* em_estfun:* gb_est5:* gb_est4:* em_gss_pro:* em_gss_other:* 0.5 7.0 7.0 32308132

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 4 | 1 4 | A 4 | 4.7 | 42 | 41 | 40 | 39 | 38 | 3/ | 36 | , (| J (| ى ر - د | 2 0 | ب د د | . · | ۱ د | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | c 19 | 18 | c 17 | 16 | · 15 | 14 | 13 | 12 | 11 | 10 | 9 | œ | 7 | б | 5 | 4 | ω | 2 | 1 | Result No. |
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| 4 | 1 6 | <u>-</u> | 4 5 6 | 457 | _ | 459.5 | 460 | 460 | 460.5 | 9 | 401 | 7.2 | 104.0 | 2 | * 4 7 0 | | 482 5 | _ | 488.5 | _ | 498.5 | 499 | 499 | 501 | 504 | 510 | 519 | 545 | 548 | 548.5 | ı n | 570.5 | \mathbf{a} | \mathbf{a} | 619.5 | 631 | 31 | 7: | 46 | 72 | 58 | 832.5 | 5 | 54 | 77 | w | Score |
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| ě | 9 | 9 6 | י כ | ÷ | f | 46 | 60 | RS | 60 | BI829118 603079231 | Ü | i e | 6 | 2 5 | 3 6 | 35 | 7 | 2 | 3 : | 5 | BB653397 | 60307 | 6 | \subseteq | ₹ | BF937654 fm67c05.y | ⊆. | L57: | pgr | IL.O | Homo s | AL539373 AL539373 . | Homo s | U13322 | ij | L538200 | Mus | AGENC | 6024 | ·ID | di- | Homo | Mus mus | AV729 | UI-M-E | AU169868 AU169868 | Description |

ALIGNMENTS

| REFERENCE | VERSION KEYWORDS SOURCE ORGANISM | RESULT 1 AU169868 LOCUS DEFINITION ACCESSION |
|---|---|--|
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias. 1 (bases 1 to 662) | AU169868.1 GI:12591937 EST. Japanese medaka. Oryzias latipes | AU169868 662 bp mRNA linear EST 29-JAN-2001 AU169868 Ol-br-ad cDNA Oryzias latipes cDNA clone br5332, mRNA Sequence. |

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Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Mita K
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/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
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/strain="HNI"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections to the collections of the 
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/dev_stage="embryo 15.5 dpc"
/lab_host="hH10B (TI phage resistant)"
/note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I;
/note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
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/strain="C57BL/6"
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US-10-075-846-4 (1-431)

x BQ443713 (1-779)

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RESULT 3
AV729257
LOCUS
DEFINITION
ACCESSION
                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                             REFERENCE
                                                                                                                    AUTHORS
Homo sapiens CDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome
351 Guo Shoujing Road, Zhangji
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                          687
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AV729257 HTC
AV729257
AV729257.1
EST.
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                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 678)

Huang, O., Yang, Y., Gao, G.,
                                                                                 Gu,Y., Peng,Y., Song,H., Huang,Q.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,
,S., Gu,W., Tu,Y., Jia,J., Fu,G., F
Chen,J., Chen,Z. and Han,Z.
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                                                                                                                                                                                                                                                                             GluAspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIle
                                                                                                                                                                                                                                                                                                        GATCCCTCAATGTTGGATTTGGAAACCGGATTTGTTCTTTGCCAATGAAAAGGGT
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                                                                                                                                                                                                               sapiens
                               Genome Center at Shanghai
Zhangjiang Hi-Tech Park,
                                                                                                                                                                                                               678 bp mRNA linear cDNA clone HTCCHE03 5',
                                                                                              Ren,S.,
                                                                                            Yang,Y., Gao,G., Xiao,H., Xu,X
,X., Cheng,Z., Xu,Z., Zeng,L.,
Ren,S., Zhong,M., Lu,G., Hu,R.,
                                                                                                                                        Hominidae;
                                 Pudong,
                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                  Euteleostomi;
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                                  Shanghai
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Query Match:
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This clone is available
                                                                                                                                                                                                               TTGGC
                                                                                                                                         ThrCysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTCTGCAAAGACCATGACTCCAGGTCTGGAAAACAACCTTCACAGACCCTATCTCCT
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                       euGlyCysCysThrLysHisTyrAsnThrGly
                                            GTGCAAGTTGCTGAAAGATTGACCCTTGCCCAAGGTTATTTTGAAAGAAGACGACGGACC
                                                    ---AGTTTTGGGTACACGATGAATGACCTGATATTTGAGTGGTTAAGTGATGGTCCA
                                                                                              LeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAla
                                                                                                                              ACCTGTACAATGCAGCTGGAG----
                                                                                                                                                                       ArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCCHE03"
/clone_lib="HTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript sk(-); Site_1:
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854.50
81.03%
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37.94%
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Matches:
Conservative:
Mismatches:
Indels:
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AUTHORS
TITLE
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                     41
                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 54 Row: 1 Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1414967 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyl
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
.cDNA Library Preparation: Life Technologies, Inc.
.cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2991)
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                                                                            LysGluGluValLysSerGlyThrLysGlySerGln
                                                                                                              ATCTCCTTTTTTTTTTATTTAATGTCCTTG-
                                             AAAGAAAAGTCTTCCAAGAAAGGGAAGGGGAAAAAGAAGCAGTACTTGTGCCCCATCCAGT
                                                                                                                                        LeuSerPheLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAlaLeuAla
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                                                                                                                                                                                                                                                                                                                                             /tissue_type="Eye, retina, mo/clone_lib="NIH_MGC_94"
/lab_host="DHIDB"
/note="vector: pCMV-sPORT6"
a 587 c 607 g 920 t
                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5360070"
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853.50
64.10%
48.21%
37.90%
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CTG-----GTCAGTTATGATCCCAGGATCAGACCAAACTTCAAAGGCATTCCTGTT
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                                                                                                                                           AlaLeuLeuGluTyrAlaAlaIle------AsnPheValSerArgGlnHisLys
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                                                                                       GluPheIleArgLeuArgArgArgGlnArg
                                                                                                                        TCCCTCGTGGAGTACGCTGTGGTCCAGGTGATGCTGAACAATCCCAAAAGGGTTGAAGCC
                                                                                                                                                                                       AGGAGACAGGTTGGGTTCTACATGATGGGCGTATATGCACCAACCTTGCTGATTGTGGTT
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| CAGCAGTCAGCAGAGGACCTTGCCCGAGTACCTGCCAACTCCACCTAGCAATATCTTGAAC LyśLeuMetGlyArgThrSerGlyTyrAspAlaArg1leArgProAsnPheLysGlyPro ::: ::: AGGTTATTGGTCAGTTATGATCCCAGGATAAGCCAAACTTCAAAGGCATT | AlaLysGluGluValLysSerGlyThrLysGlySerGlnProMet | ThrLeuSerPheLeuLeuLeu ::: ::: ACAACTGCCTTTTTAATTTT | 36.97% Indels: 11 Gaps: 6-4 (1-431) x RC022502 (1-2593) | Scores: 1.54e-94 Length: 2593 milarity: 63.78% Conservative: 64 Similarity: 47.45% Mismarthes: 89 | 824 a | /tissue_type="Brain, hypothalamus" /clone_lib="NIH_MGC_96" /lab_host="DH10B" | | • | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19 This clone was solected for full length sequenting because it | tact: (Dicks kson, M., Sch | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu | Email: cgapbs remail.nih.gov Email: cgapbs remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshivuki and Piero Carninci (PIKEN) | Bethesda, MD 201 | Strausberg,R. Strausberg,R. Direct Submission Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MCC), Cancer Genomics Office, National Cancer | Homo saplens Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2593) | |
| RESULT 6 BE981841 LOCUS DEFINITION ACCESSION VERSION KEYWORDS | Qy Db | Qy Db | Оy | Qy Db | Qy | Qy Db | Qy Db | . Qy Db | Qy Db | Qy Db | Qy Db | Qy . Db | Qy Db | Qy | Ф | Qy Db |
| BE981841 OUI-M-CG0p-bdd-h-07-0-UI.S1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bdd-h-07-0-UI 3', mRNA sequence. BE981841.1 GI:10651376 EST. | 360 HisLysGluPheIleArgLeuArgArgArgGlnArg 371 | 344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln 359 | 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343 | 304 LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 . | 284 VallleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 | 264 HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIle 283 | 245 G1yCysCysThrLysHisTyrAsnThrG1yLysPheThrCysI1eG1uValLysPhe 263 | 226 GINVALALAGIUGIYLEUTHTLEUPTOGINPHEIIELEUATGASPGIULYSASPLEU 244 ::: | 206 ServalGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaVal 225 | 186 CysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeu 205 | 166 LeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThr 185 | 146 ThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArg 165 | 126 SerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluVal 145 ::: | 108SerTyrargGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAsp 125 ::: ::: ::: ::: | 90 MetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107 | 70 ProvalasnvalThrCysAsnIlePheIleAsnSerPheSerSerValThrLysThrThr 89 ::: 335 CCTGTTGATGTAGTCAACATTTTATTAACAGTTTTGGATCCATTCAAGAAACAACA 394 |

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Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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  eLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValTh
                                                                         TTTTCTGGACAAACTAATGGGGAGGACATCGGGGTATGATGCAAGAATCAGACCCAACTT
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/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
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/db_xref="taxon:10090"
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Contact: Chin, H
National Institute of Mental Health
National Institute Blvd. Room 7N-7190, MSC
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Fax: 301 443 9890
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/organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:1090"
/clone="UI-M-GC0p-bdc-d-08-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
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| 50 LysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPheLysGlyPro 69 ::: ::: 284 AGGTTATTGGTCAGTTATGATCCCAGGATAAGACCAAACTTCAAAGGCATT 334 | 43SerProSerAspPheLeuAsp 49 | 28 AlaLysGluGluValLysSerGlyThrLysGlySerGlnProMet | | 36.97% Indels: 11 Gaps: | Pred. NO.: 1.54e-94 Length: 2593 Score: 832.50 Matches: 186 Percent Similarity: 63.78% Conservative: 64 Best Local Similarity: 47.45% Mismatches: 89 | 824 a 466 c 488 g 815 | /tissue_type="Brain, hypothalamus" /clone_lib="NHH_MGC_96" /lab_host="DH108" /note="Vector: nBluescript" | | passed the following select passed the following select This clone has the followin Location/Qualifier | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19 | | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shoc.stanford.edu | Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI) 6 Shiraki Toshivuki and Piero Carningi (PIERN) Toshivuki and Piero Carningi (PIERN) | Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, 'USA NIH-MGC Project URL: http://mgc.nci.nih.gov | J,R. (01:FEB-2002) National Institutes of Health, Mamm control (MGC), Cancer Genomics Office, National Can | HOMO Saplens HOMO Saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2593) | |
| ACCESSION VERSION KEYWORDS | RESULT 6 BE981841 LOCUS DEFINITION | Qγ | Qy Db | Qy Db | Qу | . Qy | Qy Db | Qy | ДУ | Db | Qy | . dd y | Db Qy | Qу | Qy Db | ОУ | Qy |
| | BE981841 692 bp mRNA linear EST 29-APR-2002 N UI-M-CGOp-bdd-h-07-0-UI.sl NIH_BMAP_Ret4_S2 Mus musculus cDNA clone | 360 HistysGluPheIleArgLeuArgArgArgGlnArg 371 | 344 PheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGln 359 | 324 ProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPheVal 343 | 304 LeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAlaSerLeu 323 | 284 ValileLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArgValGly 303 ::: ::: | 264 HisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeuIle 283 | 245 GlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLysPhe 263 | 226 GINVALAIAGIUGIYLEUThrLeuProGInPheIleLeuArgAspGluLysAspLeu 244 ::: ::: :::::::::: | 206 SerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaVal 225 | 186 CysThrMetGlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeu 205 | 166 LeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThr 185 | 146 ThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSerIleArg 165 | 126 SerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHisGluVal 145 ::: | 108SerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMetLeuAsp 125 | 90 MetAspTyrArgVálAsnValPheLeuArgGlnGlnTrpAsnAspProArgLeu 107 | 70 ProValasnValThrCysAsnIlePheIleAsnSerPheSerSerValThrLysThrThr 89 ::: ::: 335 CCTGTTGATGTAGTCAACATTTTTATTAACAGTTTTGGATCCATTCAAGAAACAACA 394 |

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Fax: 301 443 9890
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                        eLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSerSerValTh
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac 
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/clone="UI-M-CG0p-bdd-h-07-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
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                                                                                                                                                                                                                                   considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
                                                                                                                                                                                                                                                                                                       Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, 20892-9643, USA
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Bonaldo, M.F., Lenno
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                                                                                                                                                                                  Seq primer: M13 Forward POLYA=No.
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                                                /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UI-M-CG0p-bdc-d-08-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
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National Institutes of Health, Mammallan
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High quality sequence stop: 808
Location/Qualifiers
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Tissue Procurement: The Cepko Laboratory
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AGENCOURT_8930535
5', mRNA sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13990 row: p column: 20
High quality sequence stop: 638.
Location/Qualifiers
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Tissue Procurement: The Cepko Laboratory
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BQ938794
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National Institutes of Health, Mammalian
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                                                                                                            /organism="Mus musculus"
/db_xref="Taxon:10090"
/clone="IMAGE:6466531"
/clone_1ib="NHH_MGC_94"
/tlssue_type="retina"
/lab_host="DH10B (Phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
63 a 234 c 221 g 257 t
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                            2475 bp mRNA linear HTC 19-, Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900059Al5:gamma-aminobutyric acid receptor, subunit alpha 4, full insert sequence AK013727
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                                                        Adachi, ..., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Tagami, M., Tagawa, A., Taskahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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Fax:81-45-503-9216)
AlaThrLeuSerPheLeuLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAla 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB28975.1"
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LVHSESDVKSRTEVGNHSSKTSAVQESSEATPKAHLASSPNPFSRANAAETMSAAARG
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SSLVQYDLIGQTVSSETIKSITGEYIVMTVYFHLRRKMGYFMIQTYIPCIMTVILSQV
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/dev_stage="adult"
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| 1574 | CAAAAAGAAGATATCAAA | |
| 381 | 362 GluPheIleArgLeuArgArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGln | |
| 1526 | - | |
| 361 | 342 PheValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLys | |
| 341 1484 | 322 SerLeuProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeu : | |
| 321 1424 | 302 ValGlyLeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgAla 3 | |
| 301 1364 | 282 LeuIleVallleLeuSerTrpValSerPheTrpIleAsnMetAspAlaAlaProAlaArg 3 ::: | |
| 281 1304 | 262 LysPheHisLeuGluArgGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeu 2 | |
| 261 1244 | 242 LysaspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluVal 2 ::: | • |
| 241 1187 | 223 ProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAspGlu 2 ::: ::: ::: | |
| 222 1127 | 204 SerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGluAspAla 2 | |
| 203 | 184 GInThrcysThrMetGInLeuGIuSerSerSerIleLeuCysSerProLeuProSerLeu 2 | |
| 0 0 | 4 IleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysA ::: | |
| 163 989 | 144 GluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGlyAsnValLeuTyrSer 1 ::: | |
| 143 929 | 124 LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 1 ::: ::: | |
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| 103 812 | 84 ServalThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn 1 ::: ::::: | |
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| 53 592 | 47 PheLeuAspLysLeuMetGLyArgThrSerGlyTyrAspAlaArgIleArg 6 | |
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_FL013_FBrn1"
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               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Rodentia;
  MGC
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                                                                                                                                                                                                                                                                  SerSerValThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrp 102
|||::: :::|||||||||||||||||||||||||:::|||
GGATCCATTCAAGAGACAACAATGGACTATAGAGTTAACATTTTCTTGAGACAGAAATGG 295
GlyAlaAsnPheHisGluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGly
                                                                                                                                                                                                                                                                                                                                                                   LeuAspProSerMetLeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLys 138
                                                                                                                                                                                                            AsnAspProArgLeu-----SerTyrArgGluTyrProAspAspSerLeuAsp
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                                                                          GTTGACCCCACCATGTATAAGTGCTTGTGGAAACCTGACTTATTCTTTGCAAATGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole brain"
//dev_stage="embryo 18.5 dpc"
/lab_host="DH108 (T1 phage resistant)"
/lab_host="DH108 (T1 phage resistant)"
/lab_host="DH108 (T1 phage resistant)"
/lote="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/lote="Organ: brain organ: brain on a l% agarose of a ly organ: brain of a ly organism organism of a ly organism organ
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                                                                                                                                                           source
                                                                                                                                                                                                                                                            ,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 29
Tel: 81-438-52-3975
Fax: 81-438-52-3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                              Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Saito, K.,
,S., Masuh
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AU133223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       HRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 817)
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                                                                                                                                                                                                                                                                                                                                                                    human cDNA project (Ota,T., Sugiy
to,K., Yamamoto,J., Nishikawa,T.,
, Masuho,Y., Isogai,T.)
                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugiyama, T., Ishii, S.,
                 /note="Vector: pME18SFL3; mRNA from NT2 neuronal cells after 2-weeks retinoic acid (RA) induction" a 207 c 198 g 202 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NT2RP4
                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP4001569"
/clone_lib="NT2RP4"
                                                                /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:10993762
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Homo sapiens
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a,T., Nakamura,Y., Nagai,T., Sugano
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                                                                                                                                                                                                                                                                                            Japan
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1942 bp mRNA linear HTC Homo sapiens, gamma-aminobutyric acid (GABA) A receptor, clone IMAGE:5178575, mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Proparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (06-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hüly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                    ATTCTCAACAAGTTGCTAAGAGAA-----
                                                PheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArgProAsnPhe
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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/clone="IMAGE:5178575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="LocusID:2567"
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AL539373
AL539373.1
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 948)
                                                                                                                                                AL539373 LTI_FL013_FBrn1
                                                                   human.
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| Оу 16 | Db 4 | Оу 144 | Oy 124 Db 411 | Oy 104 Db 354 | Оу (Db 29 | Оу (Db 2: | Oy . | . Qy 2 . Db 12 | Qy 1 Db 6 | US-10-075-8 | Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match: DB: | BASE COUNT | FEATURES Source | AUTHORS TITLE JOURNAL COMMENT |
|--|----------------------------|--|---|--|---|--|--|--|--|----------------------------------|---|--|------------------------|--|
| 4 IleArgLeuThrLeuIleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIle 183 | CAGTGAAAAATCGAATGATTCGACTG | GluValThrThrAspAsnLysLeuLeuArgIlePheLysAsnGl | 24 LeuAspSerIleTrpLysProAspLeuPhePheAlaAsnGluLysGlyAlaAsnPheHis 143 | .04 AspProArgLeuSerTyrArgGluTyrProAspAspSerLeuAspLeuAspProSerMet 123 | 84 ServalThrLysThrThrMetAspTyrArgValAsnValPheLeuArgGlnGlnTrpAsn 103 ::::: ::: ::: ::: | 64 ProAsnPheLysGlyProProValAsnValThrCysAsnIlePheIleAsnSerPheSer 83 | 46AspPheLeuAspLysLeuMetGlyArgThrSerGlyTyrAspAlaArgIleArg 63 :::: ::: ::: | 7 LeuAlaLysGluGluValLysSerGlyThrLysGlySerGlnProMetSerProSer 45 | .0 SerPheLeuLeuTrpThrLeuProGlyGlnValLeuLeuArgValAla 26 | 146-4 (1-431) x AL539373 (1-948) | Ores: 1.03e-61 Length: 948 570.50 Matches: 121 Llarity: 57.64% Conservative: 60 imilarity: 38.54% Mismatches: 108 25.33% Indels: 25 Gaps: 6 | 9606" 9606" YM17" YM17" PG tiss d 26 we d 26 we d 26 we tal bra with a with a with a with a tal be-st the Not the Not the Si OSA F Com URL | cope.cns.fr, ualifiers | 1 m 0 m |

| 184 GlnThrCysThrMetGlnLeuGluSerSerSerIeLeuCysSerProLeuProSerLeu 203 |
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Search completed: July 1, 2003, 00:55:27 Job time: 2277.88 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US10075846/runat_25062003_163648_5147/app_query.fasta_1.782
-Q-/cgn2_1/USPTO_spool/US10075846/runat_25062003_163648_5147/app_query.fasta_1.782
-DB--GenEmbl -OEMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTEMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-200000000
-USER-US10075846_@CGN_1_1_3854_@runat_25062003_163648_5147 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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36: em_htg_vrt:*
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38: em_sy:*
40: em_htgo_nus:*
41: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. O 0000 იი C 0000 000 00 C Score Query Match Length 598 3.3 139754 3.3 1647754 3.3 174354 3.3 193627 3.3 197769 3.3 2197769 3.3 2197769 3.3 2197769 3.3 2197769 14309 69740 85149 1061628 113704 113704 113704 113705 112062 1121705 1 39796 39796 170676 183125 189127 195477 195477 91582 169845 169845 172555 BG GG126MRP AC11837 AC095184 AC108830 AC124635 AC124635 AC094182 AC125309 AC1273729 AC1273729 AC1273729 AC087748 AC008748 AC087748 AC068748 AC08748 AC118805 AC18805 AC188 AX037570 HSU35G3 AC026258 AP00284114 AC079196 AC079196 AC1098732 AC095732 AC095732 AC095220 AC102866 ID. AC094114 AC079196 AC109887 AC094926 AC094926 AC095220 AC0951816 AC118327 AC118327 AC118327 AC118327 AC118327 AC118327 AC118327 AC118327 AC008891 AL1353724 AC118360 APD02984 AC118805 AC018807 AC068786 AC099748 AC10901 AC111125 AC104396 AC1 AE000738 AC087748 AL137879 AC105876 Description 309 Mus muscu 336 Mus muscu 729 Mus muscu 125 Mus muscu 396 Mus muscu 987 Rattus no 201 Mus muscu 0 S.pombe chr 1 H. sapiens 738 Aquifex a 748 Homo sapi 879 Human DNA 876 Rattus no 9 Human DNA s 310 Equus cab)72 Sequence 2 Human perox Human DNA Rattus no Homo sapi Rattus no Homo sapi Homo sapi Homo sapi Homo sapi Rattus no Homo sapi Homo sapi Rattus no Rattus no Rattus no Rattus no Mus muscu Rattus no luman DNA s Homo sapi Homo sapi

ALIGNMENTS

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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-APR 1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is the entire insert of clone U35G3. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX037570 39796 bp
Sequence 6 from Patent WO0058461.
AX037570
                                                                                                                                                                                The true left end of clone U35G3 is at 1 in this sequence. right end of clone U35G3 is at 39796.
U35G3 is from the Lawrence Livermore National Laboratory flow-sorted X chromosome cosmid library LLOXNCO1.
                                                                                                                                                                                                                                                                                                       annotated human repeat sequence elements (e.g. Alu). Where is an annotation using the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 39796)
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DXS87 on chromosome
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                                                                                                                                                                                                                                                                                    feature key
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HOERBRAND GUDRUN (DE)
Location/Qualifiers
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/db_xref="taxon:9606"
9337 c 9355 g 1047
       /clone="LL0xNC01-35G3"
/clone_lib="LL0xNC01"
                                                     /map="X"
                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                           'chromosome="X"
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Conservative:
Mismatches:
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                          /note="L1MB8 repeat: matches 413.
31110. .31403
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1267. .1477
note="MIR repeat: matches 1. ..
/note="AluSq repeat: matches
                                                                                                /note="AluSg repeat:
incomplete repeat"
30706..30781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20456. .20696
/note="AluSx repeat: matches 44.
incomplete repeat"
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/note="LIPA6 repeat: matches 571. .457 of consensus"
                                                                                                                                                                                        /note="AluSg repeat:
incomplete repeat"
                                                                                                                                                                                                                                                         /note="AluJo repeat:
incomplete repeat"
                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 31.
                                                                                                                                                                                                                                                                                                                                                     'note="MIR repeat: matches 49. .196 of consensus"
27270. .27486
                                                                                                                                                                                                                                                                                                                                                                                                                         'note="FLAM_A repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR2 repeat: matches 16. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 20. .162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluJb repeat: matches 295. .1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l6847. .17148
/note="AluSq repeat:
l7947. .18235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="MIR repeat:
14745. .14874
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/note="MIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSp repeat: matches 303. .1 of
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5054. .25347
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22729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .156 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .19 of consensus"
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                                                                                                                                                                                                                                                                                                                             250 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .189 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .146 of
  .293 of consensus"
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                                                .676 of consensus
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RESULT 3
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                                                                                                                Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand,Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 170676)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170676 bp Homo sapiens chromosome 8, clone AC026258
                                     Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamacrares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
                                                                                                                                                                                Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                      Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
                                                                                                                                                                                                                                                               Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                         Jnpublished
                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome
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<38771...>39796
/note="match: 5' EST C16803 clone GEN-530B01; match: 5'
EST C16720 clone GEN-522A09; match: 5' EST C17570 clone
GEN-549E01"
<a href="match: 5" EST T86096 clone 114200; match: 3' EST
W67655 clone 343194"</a>
<a href="match: 5" EST T86096 clone 114200; match: 3' EST</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat: matches 105. 37468. 38250
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/note="AluSg repeat:
incomplete repeat"
36958 .37110
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                  Meneus,L.,
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Mihova,T., Miranda,C., Mlenga,V., Morrow,J.
Norman,C.H., O'Connor,T., O'Donnell,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 365.
                                                                                                                                                                                                                                                                                                                           8, clone
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Matches:
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                                                                                                                                                                                                                                                                                                                         and Lander, E. RP11-67N21
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RP11-67N21, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRI 18-AUG-2001
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O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Phunkhang,P., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Rieback,M., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Troub, C., LaRocque, K., Lamazares, R., Landers, T., Landers, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L7482 Center clone name: 67_N_21
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                                                                                            /rpt_family="MLT1J1"
complement/200,
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                                                                                                                                                                                                                                                     /rpt_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="L1MEd"
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repeat_region

rpt_famil

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8672. .8719
                                                                                                                                                                                                                                  complement(19826. .20188)
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/rpt_family="L2"
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4951. .5281
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                                                                                            _family="(TG)n"
5. .23830
                                                                                                                                          _family="MER69"
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3. .27289
                                                                          family="MIR"
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                               family="(TA)n"
. .25500
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Best Local Similarity:
Query Match:
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                                                                                                                     Direct Submission
Submitted (10-AUG-2000) Nobuyoshi Shimizu, Keio University, Sc
Submitted, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
On Jan 19, 2001 this sequence version replaced gi:9798632.
                                                                                                                                                                                                               Published Only in DataBase (2000) In press 2 (bases 1 to 183125) Shimizu,N. and Asakawa,S.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 183125) Shimizu,N. and Asakawa,S. Homo sapiens chromosome clone KB1670H7 on 8q23
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens genomic DNA, AP002848
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33152, .33240
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complement(33832.
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/rpt_family="MIR"
27834. .28144
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complement(27340.
/rpt_family="L2"
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/db_xref="taxon:9606"
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/rpt_family="MIR3"
                              /map="8q23"
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/rpt_family="L2"
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28499. .28616
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complement/accord
cell_line="FLEB 14 -
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_family="L2"

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family="L2"

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| er er | /ppt_family="MLTIA2" /rpt_family="MLTIA2" 17596. 17878 /evidence=not_experimental /rpt_family="MLT2E" complement(17884. 18823) | 17054. 17186 /evidence-not_experimental /rpt_family="MLT2E" 17187. 17595 | <pre>complement(13994tolit) /evidence=not_experimental /rpt_family="MLTIB" 1674616902 /evidence=not_experimental /evidence=not_experimental</pre> | M M M M | /FPC_ramily="LA" 14920. 14998 /evidence=not_experimental /evf_family="MITH" complement(15176. 15653) | /evamence-not_experimental /rpt_family="MiR" complement(1457914677) /evidence-not_experimental | /evidence-not_experimental /rpt_family="L2" /complement(1430714557) | /evidence=not_experimental /rpt_family="(TC)n" complement(1375213836) /evidence=not_experimental /rpt_family="MIR" complement(1369 14098) | /rpt_ram.ty="LZ" 1176. 11956 /evidence=not_experimental /rpt_family="MIR" 13212. 13232 | /evidence-not_experimental /rpt_family="AluSx" 10799. 10895 /evidence-not_experimental | /rpt_family="MIR" 1018210506 /evidence=not_experimental /rpt_family="L2" 1050710798 | <pre>complement(72158911) /evidence=not_experimental /rpt_family="HERVL" complement(98249923) /evidence=not_experimental</pre> | complement(56515736) /evidence=not_experimental /rpt_family="12" complement(58707113) /evidence=not_experimental /rpt_family="12" /rpt_family="12" /rpt_family="12" | <pre>/clone_lib="Keio BAC library" complement(119, .1004) /evidence=not_experimental /rpt_family="Lipal3"</pre> |
| repeat_region repeat_region | repeat_region repeat_region | repeat_region | repeat_region | repeat_region repeat_region | repeat_region repeat_region | | repeat_region | repeat_region repeat_region | repeat_region repeat_region | | repeat_region repeat_region | | | repeat_region repeat_region |
| <pre>/rpt_family="MIR" /rpt_family="MIR" complement(3341433633) /evidence=not_experimental /rpt_family="MIR" complement(3378234282)</pre> | 1184. 31512 31884. 31512 /evidence=not_experimental /rpt_family="L2" 32561. 32348 32561. 32348 | /evidence=not_experimental | /evidence=not_experimental /rpt_family="(TTTTG)n" complement(30040 30244) /evidence=not_experimental /rpt_family="MIR" /rpt_family="MIR" | /rpt_family="MER70A" 29183. 29494 /evidence-not_experimental /rpt_family="Aluy" 29731. 29753 | complement(2803828300) /evidence=not_experimental /rpt_family="MLT1K" complement(2839728851) /evidence=not_experimental | /rpt_ramily="L2" 27830. 27862 /evidence=not_experimental /rpt_family="AT_rich" | /ryt_family="L2" /rpt_family="L2" complement(2752827609) /evidence=not_experimental | /pt_family="MLT2G" 2718027403 2718027403 /evidence=not_experimental /rpt_family="MLT1J" 2741927524 /ovidence=not_experimental | 2670226766 /evidence=not_experimental /rpt_family="MLT1J" 2676727179 /evidence=not_experimental | /rpt_family="L2" /rpt_family="L2" complement(2644326521) /evidence=not_experimental /rpt_family="MADE1" | 238332873 /evidence=not_experimental /pot_family="AT_rich" 2376623825 2376623825 | B C . B C . | /evidence=not_experimental /rpt_family="tJrR16A" complement(21559, 21801) /evidence=not_experimental /rpt_family="HAL1" 22760 | <pre>complement(2041221003) /evidence=not_experimental /rpt_family="HERV16" complement(2100921269)</pre> |

Ali,A.,

Allen, N.,

Lamazares, R.,

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REFERENCE
AUTHORS
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Best Local Similarity:
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                                                                            Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Stojanovic, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stojanovi
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              Strauss, N., Tirrell, A.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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/rpt_family="LTR50"
complement(37919. .38131)
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/rpt_family="MIR"
complement(37413. .37458)
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/rpt_family="L1PA2"
complement(34414. .34574)
/evidence=not_experimental
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35473. .35652
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/rpt_family="MIR"
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/rpt_family="MLT11"
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         Subramanian, A., Tri
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12
                                                    Theodore, J.,
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         VO, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 1, 2002 this sequence version replaced gi:18450000. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferraira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., FitzHugh, W., Gage, D., Galagan, J., Gardyna, G., Galagan, G., Gal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson,B., Wu,X., Wyn
Zimmer,A. and Zody,M.
Direct Submission
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----- Genome Center
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Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. Anderson, S., Barna, N., Bastien, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-OCT-2000) Whitehead Research, 320 Charles Street, Camb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project Information Center project name: L10840 Center clone name: 1059_L_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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                                                                            /rpt_family="LlME1"
4481. .4806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-1059L18"
/clone_lib="RPCI-11 H
complement(14 .319)
                                                                                                                                                                                                                                                                                                                                                                   complement(3205.
/rpt_family="L2"
3250. .3563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1550. .2067
/rpt_family="MLT1H1"
2213. .2400
                                                                                                                                                                                                                                                                                 complement(3564
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167. .171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MLT1D" 113. .117
                                                                                                                                                                                           /rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .189127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MIR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="8"
                                                                                                                                                                                                                                                                                                                       /rpt_family="Alusx"
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                                           rpt_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Male
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/rpt_family="LIMC4"
complement(8101. 8163)
/rpt_family="LIMC2"
complement/8150
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8968 8993
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complement(8641, .8967)
/rpt_family="Alusg"
          /rpt_family="AT_rich"
complement(22383. .22538)
/rpt_family="MLT11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8994...9235)
/rpt_family="L1MC3"
9233..9440
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/rpt_family="L2"
12819 13178
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/rpt_family="LIMEC"
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/rpt_family="LlMC3"
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5477. .5791
                                                                                                                                                                                                     /rpt_family="(T)n"
complement(19989.
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/rpt_family="LTR27"
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/rpt_family="L2"
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/rpt_family="L2"
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complement(10411. .10)
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complement(683)
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complement/1500:
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complement/loss"
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complement/10707
                                                                          /rpt_family-"MIR3"
22077. .22098
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), ,)700"
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ement(7757
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                                                                                                                                                                                                   .20181)
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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Best Local Similarity:
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E2 (bases I to 195477)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Castle, A., Cooke, P., Boukpalter, B., Brown, A., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Castle, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, M., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPwan, P., McKernan, K., Pierre, N., Pisani, C., Pollara, V., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Nyan, Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J.,
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Homo sapiens chromosome 8 clone RP11-480F5 map 8, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195477)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome
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23737. 24025
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/rpt_family="MIR"
23103. .23290
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complement(28712. .28808)
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/rpt_family="MIR"
27711..27780
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/rpt_family="L2"
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24164. .24244
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zimmer, A. and Zod
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is ranks of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      earch, 320 Charles Street, Cambridge, MA 02141, USA
Nov 18, 2000 this sequence version replaced gi:9886032.
repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996–1997)
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Center clone name: 480_F
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Insert size: 193277; sum-of-contigs
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876 1876: cr
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177 1976: gap of 100 bp
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177 58986: contig of 5701
187 59086: gap of 100 b
187 60289: contig of 1203
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96530: gap of 100 bt
104817: contig of 8787
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61513: contig of 1124
61613: gap of 100 b
62903: contig of 1290
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118601: contig of 13684 k
118701: gap of 100 bp
129776: contig of 11075 k
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Rattus norvegicus clone CH230-31263,
***, 49 unordered pieces.
AC109887
Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 91582)
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,
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                                                                         Direct Submission
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                                                                                                                                  Unpublished
                                                                                                                                                        Direct Submission
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Ayele, M., Banks, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUL-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18860208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 49 contigs. The true order of the pieces
is not known and their order in this sequence record is
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L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, M., Sitson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
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Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lifeu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nickerson,E., Nwokenkwo,S., Ogah,M., Okuonu,G.,
Oragunyen,N., Nickerson,E., Nuchenkwo,S., Ogah,M., Okuonu,G.,
Oragunyen,N., Nickerson,B., Davton,B., Davton,B.,
Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-SEP-2001) Human
of Molecular and Human Genetic
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                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
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Rattus norvegicus
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Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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USA
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, *** SEQUENCING IN PROGRESS ***,
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of Medicine, One
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COMMENT
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This record w
as soon as it
be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jul 10, 2002 this sequence version replaced gi:20975871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reasonably program: Phrap; version 0.990329
Consensus quality: 104990 bases at least Q40
Consensus quality: 112511 bases at least Q30
Consensus quality: 119479 bases at least Q20
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Center clone name: CH230-
----- Summary Statis
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.
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Contact: hgsc-help@bcm.tmc.edu
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                                             Baylor Pl
On Jul 9,
                                                                            Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                      Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 191204)
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chaves
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                                                                                                                                                                                                                                                    Direct Submission
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arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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NOTE: This is a 'working draft' sequence. It currently consists of 76 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
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Chemistry: Dye-terminator Big Dye: 100% o Assembly program: Phrap; version 0.990329
Consensus quality: 128890 bases at least consensus quality: 136169 bases at least consensus quality: 141752 bases at least
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Center clone name: CH230-6B21
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Contact: hgsc-help@bcm.tmc.edu
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Allen, C., Milbrocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankeaburg, K., Bonnin, D., Barbaria, J., Benton, J., Binage, K., Blankeaburg, K., Bonnin, D., Bunks, T., Bernton, J., Binage, K., Blankeaburg, K., Bonnin, D., Bunks, T., Chen, G., Chen, R., Chen, C., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D., A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D., A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D., A., Davila, M., Douthwaite, K., J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Davila, M., Davis, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, S., Hantla, M., Hollows, C., Hollins, B., Homsi, F., Howard, S., Homeratis, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, C., Hodgson, A., Hogues, M., Hollows, C., Hollins, B., Homsi, F., Howard, S., Khan, U., King, L., Korch, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudh, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korch, J., Luu, K., Louiseged, H., Lozado, R., Lux, L., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Liu, J., Liu, M., Louiseged, H., Lozado, R., Wartin, R., Martinale, A., Martinaez, E., Mahesiwari, M., Mapua, P., Martin, R., Martindale, A., Martinaez, E., Mahesiwari, M., Mapua, P., Martin, R., Martindale, A., Mayyen, N., Wetzer, M., Martinaez, E., Mahesiwari, M., Martinaez, E., Pull, M., Wel, G., Metzer, M., Martinaez, E., Pull, M., Wel, G., Metzer, M., Peery, J., Perez, L., Perez, L., Perez, L., Perez, L., Perez, L., Perez,
                                                                                                                                                                            Direct Submission

Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

[bases 1 to 104525)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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, *** SEQUENCING IN PROGRESS ***,
Center, Depa
of Medicine,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 44880 bases at least Q40
Consensus quality: 54834 bases at least Q30
Consensus quality: 62109 bases at least Q20
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Center project name: GDJO
Center clone name: CH230-9L22
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Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Jones, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Sévery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Thomann, K., Talamas, J., Tesfaye, S., Theodore, J.,
Thomann, K., Talamas, J., Tesfaye, S., Theodore, J.,
Theodore, J
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                                                                                                                                                    On Aug 20, 2002 this sequence version replaced gi:17060976. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Plerre,M., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Phunkhang,P., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,M., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A.,
Barna,N., Barna,N., Bastien,V., Boguslavkiy,L., Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Contact: sequence_submissions@genome.wi.mit.edu
                                 Web site: http://www-seq.wi.mit.edu
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                                                                                                                                --- Genome Center
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Insert size: 171455; sum-of-contigs
Quality coverage: 12.8 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP24-576L9"
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3318. .9778
'note="assembly_fragment"
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contig of 1065
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contig of 638 bp in
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Rattus norvegicus clone CH230-501B21,
***, 30 unordered pieces.
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X61200
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Identification of genes differentially expressed in two types v-myb-transformed avian myelomonocytic cells

Oncogene 7 (3), 527-534 (1992)
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Submitted (01-AUG-1991) T.H. Graf,
AC118327
AC118327.2 GI:21747379
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/note="assembl
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198 c 129 g 113 t
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/db_xref="taxon:9031"
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                                                                                                                                                                                  Worley, K.C.
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
Li,J., Li,Z., Lichterge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucler,A., Lucler,R., Luna,R., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Moyen,N.,
Muser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,A.,
Nguyen,N., Nickerson,E., Nwokankwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pimus,E., Pullus,B., Pullus,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Syatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUL-2002) Human Genome Sequencing Centér, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA on Jul 14, 2002 this sequence version replaced gi:20149387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

3 (bases 1 to 139754)
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C
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                                                             Sequencing vector: Plasmid;
                                                                                                                                                                                              Center project name: GVZL Center clone name: CH230-501B21
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Bryant, N.P.,
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Garris, C., Harris, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, W., Harlm, Havlak, P., Hawes, A., Hennandez, J.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karlsson, E., Kelly, S., Khan, U., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Lozado, R.J., Lu, X., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H.,
Lozado, R.J., Lu, X., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Kratovic, J., Mapha, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Martin, R., Martin, R., Martindale, A., Martinez, E.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Ngyen, A., Ngyen, N.,
Ngyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pikens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Syatek, A., Tangh, P., Thomas, N., Thomas, N.,
Thomas, S.,
Usnani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. Buhay, C., Burch, P., Burkett, C., Byrd, N.C., Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Chen, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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27442 c 27265 g 3
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Conservative:
Mismatches:
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*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9049 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonnin, D.,
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Banks,T.,
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REFERENCE
AUTHORS
TITLE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17942274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 164772)
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NOTE: This is a "vorking draft' sequence. It currently consists of 85 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 79000 bases at least 040
Consensus quality: 85421 bases at least 030
Consensus quality: 90756 bases at least 020
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
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                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                     Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Mathews, C., McCarthy, M.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56522 TCTCTCTCTGTTCTCCTCTCCCCTTCCTCTCTCTCTCC 56560
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Cooke, P., Fitchugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kelis, C., LaRocque, K., Lamazares, R.,
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Mus musculus, clone RP23-232G11
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Mus musculus clone RP23-232G11,
                                                                                                                                                                                                                                           Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Birren, B., Linton, L., 
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Mammalla; Eutheria; Rodentla; Sclurognathi; Muridae; Murinae; Mus
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21 ordered
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Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On APR 25, 2002 this sequence version replaced gi:18450091. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available and the accession number will be preserved.

1 101: contig of 101 bp in length
102 201: gap of 100 bp
202 1145: contig of 944 bp in length
1146 1245: gap of 100 bp
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4067 4166: gap of 100 bp
4167 5725: contig of 1559 bp ir
5726 5825: gap of 100 hn
5826 ROTE
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Insert size: 172354; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; agarose-fp
Quality coverage: 6.0 in Q20 bases; sum-of-contigs
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Center clone name: 232_G_11
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39 8138: gap of 100 bp 11089: contig of 2951 bp in 39 11189: gap of 100 bp 90 13192: contig of 2003 bp in 913292: gap of 100 bp 11093 13292: gap of 100 bp 1
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8038: contig of 2213 bp
18138: gap of 100 hm
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2370: gap of 1025 bp in
4066: contig of 4166:
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80255 94472: contig of 14218 bp in length
94473 94572: gap of 100 bp
94573 120577: contig of 26005 bp in length
120578 120677: gap of 100 bp
120678 147069: contig of 26392 bp in length
120678 147069: contig of 26392 bp in length
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53673 66319: contig of 12647 bp in length
66320 66419: gap of 100 bp
66420 80154: contig of 13735 bp in length
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7170 174354: contig of 27185
                                                                                                                         /note="assembly_fragment"
147170. .174354
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/db_xref="taxon:10090"
/clone="RP23-232G11"
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4573. .120577
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7600. .31892
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lone_end:SP6
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6420. .80154
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5587. .53572
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6885. .20475
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1673. .66319
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12. .1145
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                                                   2055 others
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Pred. No.:

Score:

Score:

Percent Similarity:

Best Local Similarity:

The structure of t
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Search completed: July 1, 2003, 00:18:12 Job time: 249:866 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q-cgn2_1/USPTQ_spool/USI0075846/runat_25062003_163647_5141/app_query.fasta_1.782
-Q-rcgn2_1/USPTQ_spool/USI0075846/runat_25062003_163647_5141/app_query.fasta_1.782
-DB-N_Geneseq_101002 -QFM=fastap -SUFFIX=p2n.rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -USITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=USI0075846_@CGN_11_511_erunat_25062003_163647_5141 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGING
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA11981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SUMMARIES

| RESI AAC XX | 0 0 0 0 0 | 0 000000 0 | 000000000 | Result No. |
|---|---|--|---|----------------|
| SULT 1 C61681 AAC6 AAC6 19-F1 Nucli Nucli Human Homo Key exon |) A S O C A C C A S C C C C C C C C C C C C C C | 3310 3310 3310 3310 | 1 2 3 4 4 4 7 6 6 7 7 8 8 9 110 111 112 113 113 | No. |
| 1681 s 1681; 1681; EB-200 EB-200 eotide eotide n; ata sapie | 47.5 47.5 47.5 47.4 47.5 47.4 47.4 47.4 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | | Score |
| tandar 1 (fi seque seia; g | ************ | 55.55.55.55.55.55.55.55.55.55.55.55.55. | 90.7 70.7 70.7 69.3 69.3 69.3 69.3 69.3 69.3 | Query Match |
| DNA; t ent e of e the e the tag: | 10468 10468 10468 19408 19408 19408 19408 641 6641 731 | 1082 3079 1082 2667 2167 3171 3171 112460 288 289 289 668 668 668 698 730 827 4412 5412 | 39796 3294 3294 3301 3301 3301 3301 3301 3599 90 597 597 597 597 597 597 471 471 471 | Length |
| 97 97 97 97 | 222222222222 | 22222222222222222222222222222222222222 | | DB |
| ALIGNMENTS 96 BP human ataxia gene ss. aliflers 1 | AAS30512 AAS30512 AAL06288 AAL06291 AAS42003 AAK87230 AAK87230 AAK26393 AAL23844 ABL26393 AAL23844 ABK82059 ABK82060 ABK82060 | AAZZ3024 AAZZ3025 AAS74624 AAS74569 AAS75059 AAS75059 AAS75059 AAS75059 AAS75059 AAS75059 AAL16141 AAL24984 AAK68950 AAI94991 AAI94991 AAI95568 AAC195568 AAC195568 AAC195568 AAC195568 AAC195568 AAC195568 | A B B B B B B B B B B B B B B B B B B B | ID |
| | DNA encoding novel DNA encoding novel Human reproductive Human reproductive Genomic sequence # Human immune/haema Human digestive sy Drosophila melanog Human breast cance Novel floral meris Novel floral meris Novel floral meris | Rat kd312 genomic DNA encoding novel Arabidopsis thalia DNA encoding novel Arabidopsis thalia DNA encoding novel Human cDNA differe Mouse genomic regi Human breast cance Human breast cance Human breast cance Human immune/haema Human neuroblastom Arabidopsis thalia Human G-protein co Rat aorta raNBC pr Human BAI2 gene. DNA encoding novel | Nucleotide sequenc Steroid hormone re Human pPAR-delta c Lung cancer relate Human foetal liver Human foetal liver Human brain expres Probe #17300 for g Human brain expres Probe #8168 for ge Human transporter Drosophila melanog Human prostate exp | Description |

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RESULT 2
AAQ48939
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                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                          US-10-075-846-4_COPY_192_207 (1-16) x AAC61681 (1-39796)
                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                              The present sequence represents the human ataxia gene. The ataxia protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying and characterizing genetic defect involved in the disorders and diseases related to ataxia.
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AAQ48939;
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                      AAQ48939 standard;
                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acid sequence encoding human ataxia protein for screening compounds useful for treating disorders relating to mutations in ataxia
                                                                                                                                                                                                                          Sequence 39796 BP;
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-656166/63.
                                                                                                                                                                                                                                                                                                                                                                                                                  Rappold-Hoerbrand G;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (RAPP/) RAPPOLD-HOERBRAND G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000WO-EP02600
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                                                                 GCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTT
                                                                                     SerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 16
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Indels:
Gaps:
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Matches:
Conservative:
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14
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RESULT 3
AAX36523
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3294 BP; 705 A; 1014 C; 879 G; 696 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human steroid hormone receptor NUCI - used evaluate ligands binding to the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                       Nuclear receptor agonist; antagonist; identification; peroxisome proliferator activated receptor; ss.
                                                                                                                                           Human PPAR-delta coding sequence.
                                                                                                                                                                                             AAX36523;
                                                                                                                                                                                                                     AAX36523 standard; cDNA; 3301 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The steroid hormone receptor (designated NUCI) is used in assays to identify and evaluate chemical entities that bind to it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Page 6-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR41875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-305586/39.
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                                 15-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                       1837
                                                                                                                                                                                                                                                                   hormone receptor (NUCI) gene
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/product= Steroid hormone receptor
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92.86%
85.71%
70.67%
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Indels:
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06-OCT-1998;

98WO-US21049

07-OCT-1997;

97US-0061385

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RESULT 4
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-075-846-4_COPY_192_207 (1-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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05-JUN-2000

05-JUN-2000

18-SEP-2000

18-SEP-2000

20-SEP-2000

20-SEP-2000

20-SEP-2000

22-SEP-2000

22-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000

25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agonists and antagonists comprises measuring fluorescent resonance transfer between fluorescent-labelled nuclear receptors and co-activators. The method can be used for identifying agonists and
                                                                                                                                                                                                                                    Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                              Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the human peroxisome receptor-delta (PPAR-delta)
                                                                                                                                             30-MAY-2001;
                                                                                                                                                                  13-DEC-2001.
                                                                                                                                                                                     WO200194629-A2
                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                    15-MAY-2002
                                                                                                                                                                                                                                                                                                                       ABL65244
                                                                                                                                                                                                                                                                                                                                           ABL65244 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3301 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antagonist of nuclear receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for identifying nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying nuclear receptor agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-263998/22.
P-PSDB; AAY05472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cummings RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
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                                                                                                                                                                                                                                                                               cancer
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2000US-234034P.

2000US-234052P.

2000US-23450P.

2000US-234567P.

2000US-234924P.

2000US-234924P.

2000US-235077P.

2000US-235072P.
                                                                                                                                                                                                                                                                               related
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                                                                                                              2000US-209473P.
2000US-209531P.
                                                                                                                                             2001WO-US10838
                                                                                2000US-233617P.
2000US-234009P.
                                                                                                    2000US-233133P.
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Query Match:
                        Percent Similarity:
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                                                                   Pred.
                                                                              Alignment
                                                                                                                              The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61644 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. All can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a cresult of M1, and the data is sufficient to convey the chemical costructure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-SEP-2000
02-OCT-2000
02-OCT-2000
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01-NOV-2000
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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28-SEP-2000;
28-SEP-2000;
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Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 3581; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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29-SEP-2000;
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28-SEP-2000;
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                                                                   No.:
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                                                                                Scores:
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Weaver 2
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2000US-237316P.
2000US-237425P.
2000US-23759BP.
2000US-237604P.
2000US-237606P.
2000US-237608P.
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2000US-236033P.
2000US-236034P.
2000US-236109P.
2000US-236111P.
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2000US-236891P.
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2000US-237173P.
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2000US-235720P.
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US-10-075-846-4_COPY_192_207 (1-16)

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ABL65244 (1-3301)

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                               RESULT 6
                                                                                      US-10-075-846-4_COPY_192_207 (1-16)
                                                                                                                            Percent Similarity:
Best Local Similarity:
                     AAK24269/c
                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5659/c
ABA75659
                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
           AAK24269
                                                                                                                                                                                      Sequence 90
                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 23964; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                      Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA75659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human foetal liver single exon nucleic acid probe #23964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001;
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                                                                                                                    Match:
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                                                 81
           standard; DNA; 90
                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                      BP;
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                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                  C;
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                                                                                                                                                                                                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                for
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                                                                                              RESULT 7
AAI27367/
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Pred. No.:
                                                                                                                                                                                            Query Match:
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cervical cancer;
         Probe; human; microarray;
                                                                                                                                                                                                                                                                                                                                                                              brains
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Percent Similarity:
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; microarray; Alzheimer's disea
 Probe #17300
                               12-OCT-2001
                                                                                      AAI27367
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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for gene expression analysis in human cervical cell sample
                             (first entry)
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ase; multiple sclerosis; schizophrenia;
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gene expression;

cervical epithelial cell;

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US-10-075-846-4_COPY_192_207 (1-16) x AAI27367 (1-90)
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                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                               Sequence 90 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                              ABA63211 standard;
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                                                     Homo
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27-SEP-2000;
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30-JUN-2000;
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                                                                                             foetal liver single exon nucleic acid probe #11516.
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                                                                          foetal
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0234687.
                                                                                                                     (first
                                                                           liver;
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52.00
92.31%
76.92%
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                                                                                                                                                               DNA;
                                                                                                                    entry)
                                                                          gene
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                                                                         expression;
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                                                                                                                                                               ВP
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Conservative:
Mismatches:
Indels:
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                                                                          nucleic acid
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AAK11674/c
ID AAK116
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Query Match:
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK11674;
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                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
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                                                                                                                     30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                WO200157275-A2
                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11516; 639pp + sequence listing;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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2000US-0608408
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Indels:
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Matches:
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Query Match:
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
WPI; 2001-488901/53
                                                                             30-JUN-2000;
03-AUG-2000;
                                                                                              04-FEB-2000;
26-MAY-2000;
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                                                            21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                cervical
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                                                                                                                                                                                                     human; microarray; gene expression; cervical epithelial cell;
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                                 MOLECULAR DYNAMICS
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                Hanzel
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                                                           2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0236359.
2000GB-0024263.
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                                                                                                                        2001WO-US00670
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                                                   2000GB-0024263.
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                DK,
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92.31%
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                                                                                                                                                                                                                       expression analysis in
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                Chen
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                Rank DR;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                       human cervical cell sample
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                                25-FEB-2000;
02-MAR-2000;
09-MAR-2000;
17-MAR-2000;
24-MAR-2000;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7468/c
AAD17468
                                                                                                                                                                                                                                                                                             cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma; cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis; rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;
                                                                                                                    23-FEB-2001;
                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                  neurological disorder; immune disorder; allergy; nootropic; dementia; AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
          (INCY-) INCYTE
                                                                                                                                              30-AUG-2001.
                                                                                                                                                                     WO200162923-A2
                                                                                                                                                                                                                                                                                    gastritis;
                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                             10-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probe (SENP). The present sequence is one such probe. The SENPs are derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443
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                                                                                                                                                                                                                                                                                                                                                            transporter and ion channel;
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||TCGCTATCTTGCTCTCCTCTTCCCTCTGTCTCTCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA;
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                                                                                                                                                                                                                                                                                   inflammation;
                                2000US-0187947.
2000US-0188333.
2000US-0190230.
2000US-0192077.
2000US-0192077.
                                                                                                                      2001WO-US05942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B₽;
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          GENOMICS
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          INC
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                                                                                                                                                                                             "Human TRICH-1 protein"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                   (TRICH-1)
                                                                                                                                                                                                                                                                                                                                                           TRICH-1; therapy; akinesia; cardiant,
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DB:
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ID ABL03244 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport
disorders
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Khan FA,
          P-PSDB; ABB59141.
                      HPI;
                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                             23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                           Drosophila; developmental biology;
pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 4214
                                                                                                                                                                                                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                              ABL03244;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRICH-13), useful in the diagnosis, treatment and transport (e.g. akinesia), neurological, muscle or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thirteen human transporters and ion channels (referred to
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                                             Venter JC,
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                     2001-656860/75
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, Walia NK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and inflammation
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(e.g. allergies) -
                                                                   CORP NY.
                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greene
                                                                                          2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                    (first entry)
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Gandhi AR, Tribo
BD, Hernandez R,
                                           Li
                                             DWD,
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Tribouley CM, Pa
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Matches:
Conservative:
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Indels:
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RESULT 13
ABV16725/c
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Best Local Similarity:
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                                                                                                                                                                        17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryottes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511)
                                                                                                                                                                                                                                                                                                                                    Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                             ABV16725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences (ABL01840-
(ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and
                                                                                                Schlegel
                                                                                                                                                                                                                                                               23-AUG-2001
                                                                                                                                                                                                                                                                                       WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 16716
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                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE
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                                                                                                                                              2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                               Endege WO,
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                                                                                                                                                                                                                                      2001WO-US05171
                                                                                                                                                                                                                                                                                                                                    marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                   cancer; cytostatic; carcinogen; pharmacodyanamic marker;
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80.00%
66.67%
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Claim 1; Page 2785; 11750pp; English.

Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer

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Best Local Si
Query Match:
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Best Local Similarity:
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                                       Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer, stage of prostate cancer
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16-MAR-2000; 2000US-189862P
25-MAY-2000; 2000US-207454P
09-JUN-2000; 2000US-211314P
                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
              Claim
                                                                                                                                   Schlegel
                                                                                                                                                                                                                                                                                                                                                                  WO200160860-A2
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13-DEC-2000;
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              Page 9177; 11750pp;
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                                   Endege
                                                                                                                                                                                               2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; marker;
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50.00
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                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; carcinogen;
gene; ss.
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              English
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                                                                                                                                                                 MEDICINE
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
           The invention provides nucleic acid molecules encoding Kd312 polypeptides. The Kd312 polypeptides can be expresent methodology. The Kd312 sequences, and the the proteins may be used to treat or diagnose the present
                                                                                      Claim
                                                                                                                   kd312 polypeptides useful for treating diseases and disorders associated with alterations in cell proliferation and cell de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat kd312 polypeptide encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 471
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                                                                                                                                                                                                                                                                        31-MAR-1998;
                                                                                                                                                                                                                                                                                                      30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                      kd312 polypeptide;
heart attack; head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ23024;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Parkinson's
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                                                                                                                                                                               1999-601322/51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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trauma; neurodegenerative disease; rat;
e; Alzheimer's disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacodyanamic or
       ucleic acid molecules encoding human and rat
kd312 polypeptides can be expressed by standard
The kd312 sequences, and the antibodies against
to treat or diagnose the presence or progressic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1689
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                                                                                                                    cell death
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diseases,

e.g.

cancer,

or progression (e.g. AIDS), against



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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Ocqn2_1/USPTO_spool/US10075846/runat_25062003_163649_5167/app_query.fasta_1.782
-Ob=Issued_Patents_Na -OFMY=fastap -SUFFIX-p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-11 -MATRIX-blosund2 -TRANS-humand0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMY=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10075846_@CGN_1_1_84_@runat_25062003_163649_5167 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                 Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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   a
                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441362 seqs, 153338381 residues
                                                                                                                                                                                                                Query
Match Length
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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   1689
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3191
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               US-09-053-374A-4
US-09-053-374A-6
US-09-053-806-1
US-09-163-669-1
US-09-179-221D-3
US-09-453-702B-70
US-08-254-358-1
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70, Appl
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| | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 |
|---|-------------------|------------|-----|-----------|-----------------|---------------|------------|------------|---------|---------------|---------------|---------------|---------------|---------------|-------|--------------|-----------|--------------|-----------------|-----------|-----------|-----------|---|--------------|-----------------|-------------------|-----------|--------------|------|--------|------------|--------------|------|
| | 42 | | | | 43 | | 43 | ω. | 43.5 | 44 | 44 . | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 45 | 45 | 45 | 45 | | | | | | | | | 46 | | 46 |
| | 56.0 | | | | | - | 57.3 | | 58.0 | | 58.7 | 58.7 | 58.7 | 58.7 | 58.7 | | • | | • | | • | • | 60.0 | • | | • | • | • | • | • | 61.3 | • | |
| | 1168 | 1109 | 185 | 62 | 7015 | 07 | 2820 | 15 | 90 | 637 | $\frac{3}{3}$ | 12286 | 11707 | 9829 | 4609 | 2845 | 1140 | 517 | 50000 | 2976 | 2333 | 2333 | 2303 | 2234 | 1876 | 363 | 1152 | ū | 8698 | 7557 | 4910 | ū | 4910 |
| | 4 | - | 4 | 4 | 4 | S | Ŋ | 4 | 4 | w | ω | 4 | 4 | 4 | 4. | 1 | _ | 4 | 4 | 4 | 4 | 2 | w | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | 4 | Ν |
| • | US-09-484-970B-89 | -08-183-21 | σ | -729-995- | US-09-177-249-6 | T-US93-11725- | US93-11725 | 9-175-928- | -031-96 | -09-128-155-1 | -09-128-155-1 | -09-322-478-1 | -09-136-574A- | -09-322-478-1 | 22-47 | -08-289-653- | -08-289-6 | -09-288-143- | US-09-146-053-3 | -09-221-0 | -09-183-2 | -08-732-C | -289-3 | -09-087-134- | US-08-840-767-5 | US-08-580-031A-13 | s-09-103- | 09-103-840A- | | 15- | S-09-546-7 | -09-246-320- | 7 - |
| | 89, | | 11, | ω | 9 | ω | ۲, | 9 | 5, A | e 17, | 16, | 17, | ۲, | _ | 21, | 1, | e 2, 7 | e 43, | e 3, A | е 36, | e 1, | <u>ب</u> | <u>, , , , , , , , , , , , , , , , , , , </u> | 7, | 5 , | 13, | e 1, | ce 2, | Ņ | e u | e 2, Ap | e 2, Ap | e |

ALIGNMENTS

RESULT 1 US-09-053-374A-4

Sequence 4, Application US/09053374A Patent No. 6462177

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ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MAMM
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              STATE: CA
COUNTRY: US
ZIP: 91320
                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                TOPOLOGY:
                             STRANDEDNESS:
                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                          nucleic acid
TYPE:
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                linear
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                             single
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                                                                                                                                                                                                       US/09/053,374A
                                                                                                                         31,602
                                                                                           4..
                                                                                                            A-514
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GENERAL INFORMATION:

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; NAME/KEY:
; LOCATION:
US-09-053-374A-4
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                                  US-08-852-806-1
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Best Local Similarity:
Query Match:
                                                  RESULT 3
                                                                                                                                                 US-10-075-846-4_COPY_192_207 (1-16) x US-09-053-374A-6 (1-3079)
                                                                                                                                                                                                         Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                               Pred. No.:
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US-09-053-374A-6
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                                                                                                                                                                                                                                                                                               Alignment Scores:
Sequence 1, Application US/08852806 Patent No. 5874245
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-51
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARATERISTICS:
LENGTH: 3079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09053374A Patent NO. 6462177
GENERAL INFORMATION:
APPLICANT: YEN, KWANG-MU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 15 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: YEN, KWANG-MU
TITLE OF INVENTION: MAMMALIAN BLOOD LOSS-INDUCED GENE, KD312
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                  237 TCCGGCGCCCTCTGCAGCCCTCTACCTTCTCTCAGC 272
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US-09-163-669-1
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/017,91
FILING DATE: 16 MAY 1996
ATTOREY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REGISTRATION INFORMATION:
TELECOMBUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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ANTI-SENSE: NO
FRAGMENT TYPE:
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STATE: F.
COUNTRY: U.S.A.
*TP: 19406-0939
*TP: PADABLE F.
**TP: TOTAL COUNTRY: TOTAL COUNTRY: TOTAL COUNTRY: TOTAL COUNTRY COUNTR
                             CORRESPONDENCE ADDRESS:
                                                                  TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTOR (HIBCD07) NUMBER OF SEQUENCES: 14
                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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APPLICANT: Shuji Hinuma
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                           APPLICANT:
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   ADDRESSEE:
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

COUNTRY: U

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Valley Forge PA

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Alignment Scores:
                                                                                 US-09-535-008-40
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Best Local Similarity:
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TELEY: 846169

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

SEQUENCE 3271 base pairs
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APPLICANT: Wong, Alexander K.C.
APPLICANT: Taytigian, Sean V.
APPLICANT: Taytigian, Sean V.
APPLICANT: T
                                                                                                          EARLIER APPLICATION NUMBER: U.S. 60/125,806
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
LENGTH: 724
TYPE: DNA
ORGANISM: Homo sapiens
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NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: TAK-50002-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
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APPLICATION NUMBER: 08/852,806
FILING DATE: 07-MAY-1997
APPLICATION NUMBER: 60/017,915
FILING DATE: 16-MAY-1996
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OPERATING SYSTEM: DOS
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US-09-179-221D-3/c
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Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 70, Application US/09453702B Patent No. 6365723
GENERAL INFORMATION:
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APPLICANT: Musso, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID SEQUENCES DIAGNOSTIC FOR PATHOGENIC E.
TITLE OF INVENTION: COLI 0157, METHODS OF IDENTIFICATION AND KIT THEREFOR
FILE REFERENCE: 922.6496p
CURRENT APPLICATION NUMBER: US/09/179,221D
CURRENT FILING DATE: 1998-10-27
NUMBER OF SEQ 1D NOS: 16
SOFTWARE: No. 6291168epad
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ORGANISM: E.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.4
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Word Perfect 8.0
CURRENT APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                               TITLE OF INVENTION: NO. 6365723el Sequences NUMBER OF SEQUENCES: 265
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                                                                                                                                        COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                          CITY: Madison
STATE: WI
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                                                                                                                                                                                                                                                                                                              Guy
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Matches:
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Indels:
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                                                                                                        1.44Mb storage
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Best Local Similarity:
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                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Johnson, Phi.
TITLE OF INVENTION: Met.
TITLE OF INVENTION: Met.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5658785and, Greta E.
NAME: NO. 10058ER: 35,302
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 0300
CITY: Chicago
STRANDEDNESS
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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TELEFAX: (608) 251-9166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
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STRANDEDNESS: double
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Adeno-Associated Virus Materials
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Matches:
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US-10-075-846-4_COPY_192_207 (1-16) x US-08-475-391-1 (1-4680)
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                                                    Query Match:
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Query Match:
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APPLICANT: Johnson,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-JUN-1:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 01
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDING STREET: DJ. CITY: Chicago STATE: Illinois STATE: USA
                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: No. 5786211and, Gr
                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 474-634
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
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                                                    Mismatches:
Indels:
                                                                                     Matches:
Conservative:
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PCT-US95-07178-1
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Query Match:
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US-08-709-609-1
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                                                                                                                                                  Sequence 1, Application PC/TUSYDU GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
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APPLICANT: Johnso
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: Adei
TITLE OF INVENTION: Meti
TITLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
STREET: CLICAGO
CITY: Chicago
Illinois
                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: No. 5858775and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                  ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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6300 Sears Tower, 233 S. Wacker Drive
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Adeno-Associated Virus Materials and
                                                                                                                     Methods
                                                                                                                                      Adeno-Associated Virus Materials and
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RESULT 12
US-08-331-384-2/c
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                ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fisher, TITLE OF INVENTION: TITLE OF INVENTION:
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NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,
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                                                                                                                      CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (312) 474-630
TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                         CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                               STREET:
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                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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REFERENCE/DOCKET NUMBER: UPNG1149USA
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William M.
Krishna J.
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                                                                                                    US/08/331,384
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                                                                                                                                    Version
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TELEPHONE: 215

215-540-9200

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RESULT 13
US-08-836-087-2/c
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; MOLECULE TYPE:
JS-08-836-087-2
                                          TELEFAX: 215-34 C.: 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4910 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Patent No. 5871982
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                          REFERENCE/DOCKET NUMBER: GN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                         APPLICATION NUMBER: 08/331,384 FILING DATE: 28-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LENGTH: 4910 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Spring House
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                                                                                                                                                                                       REGISTRATION NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                TOPOLOGY:
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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Fisher, Krishna J.
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US-10-075-846-4_COPY_192_207 (1-16) x US-09-246-320-2 (1-4910)
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Best Local Similarity:
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                                                                                              Query Match:
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                                                                                                                                              Score:
                                                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-540-5818 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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No.:
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TOPOLOGY: unl
MOLECULE TYPE:
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TELEFAX: 215-540-5818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                  LENGTH: 4910 base pairs
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1 SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer 15
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Spring House Corpora
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WENTION: Hybrid Adenovirus-AAV Vector and
NVENTION: Methods of Use Thereof
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Kelley, William M.
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Matches:
Conservative:
                                                                                                                                            Length:
Matches:
                                                                              Gaps:
                                                                                             Mismatches:
Indels:
                                                                                                                            Conservative:
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2062 ACATCCCCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGT 2018

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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-546-738-2/c
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Search completed: July 1, 2003, 00:57:37 Job time: 12.4004 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GNVPN.007PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-540-9200
TELEFAX: 215-540-9200
TELEFAX: 215-940-9818
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4910 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Patent NO. 6387368
GENERAL INFORMATION:
APPLICANT: Trustees of University of Pennsylvania
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,738
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: ADATA:

OPERATOR OF THE PROPERTY OF
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Kelley, William M.
Fisher, Krishna J.
TITLE OF INVENTION: Hybrid Adenovirus-AAV Vector and
Methods of Use Thereof
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ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
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NAME: Bak, Mary E.
                                                                                                                                                                              2062 ACATCCCCAATTACTTGCTCCCCAAAACCCAGCCTGAGCTCCAGT 2018
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                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/246,320 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Spring House
STATE: Pennsylvania
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46.00
73.33%
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61.33%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -Q-/cgn2_1/USPTO_spool/US10075846/runat_25062003_163649_5181/app_query.fasta_1.782
-DB-Published_Applications_NA -OFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -NATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US10075846_@CGN_1_1_102_@runat_25062003_163649_5181
-NCPU-6 -TCPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS=1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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-MODEL-frame+_p2n.model -DEV-xlp
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Maximum DB
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Sequence:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
  100.0
70.7
70.7
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW.PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW.PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW.PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
    1640
2982
3301
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US-10-075-846-3
US-09-938-842A-93
US-09-954-456-554
US-09-864-761-30015
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2788.018 Million cell updates/sec
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                                                                                                        Description
                                      Sequence 3, Appli
Sequence 93, Appl
Sequence 554, App
Sequence 30015, A
                                                                                                                                                                                                                                      printed,
                                         Alignment Scores: Pred. No.:
                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(1293)
US-10-075-846-3
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                      Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10075846 Publication No. US20030032608A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                               SEQ ID NO 3
                                                                                                                                                                      LENGTH: 1640
TYPE: DNA
ORGANISM: homo s
FEATURE:
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 81
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| 4 4 | ω | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | | ø | 80 | 7 | σ | σ |
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| 46 | 4.0 | 40 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | | 46 | 46 | 46 | 46 | . 46 | 46 | 46 | | 46 | 46 | 46 | 46 | 47 | 47 | 47 | 47 | 47 | 47 | 47 | 48 | 48 | 48 | 48 | 48 | 48 | 48 | 49 | 52 |
| 61.3 | ٠. | ۲ | 1. | Ξ. | Ι. | 1 | Ξ. | | 7 | | 61.3 | 1. | Ϊ. | : | 1. | 61.3 | 1. | 1 | 1. | 61.3 | : | 1. | 1. | 2.7 | 2.7 | 62.7 | | 62.7 | 62.7 | 2 | ٠. | 64.0 | 64.0 | 4. | 4 | 4. | 4. | 5.3 | 9.3 |
| 1866 | 1866 | 1866 | 1866 | 1866 | 1866 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1611 | 1591 | 1363 | 479 | 424 | 408 | 289 | 254 | 231 | 465237 | 174424 | 110079 | 4000 | 771 | 381 | 263 | 10468 | 10468 | 5399 | 791 | 720 | 576 | 497 | 249487 | |
| 9 9 | o o | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 9 | 10 | 10 | 10 | 10 | 9 | 9 | 9 | 10 | 10 | 10 | 9 | 10 | 9 | 10 | φ | ø | φ | 9 | 9 | 9 | 10 | 10 | 9 | 10 |
| US-10-082-671-8 | -09-953-351 | -10-080-376- | -10-080-376- | 792-630- | -09-792-630- | 097-100-1 | 097-100- | 082-671 | 82-671- | -351 | -09-953-351 | | -376- | 792-630- | 09-792-630- | 5-300 | 880-192- | -09-864-761-1 | US-09-783-590-2728 | 09-918-995-23 | -09-991-936- | 28-444-3 | -09-864- | 09-933-2 | 967- | US-10-175-523-96 | 8-09-8 | 09-764-891-7 | S-09-983-965-394 | 18-995-307 | 764-891-897 | 764-891 | US-10-225-567A-343 | 8-846-724 | 10-198-846-128 | -09-974-300-86 | S-09-783-5 | 026-188 | S-09-864-7 |
| Sequence 8, Appli | 'n | ۵, | Ņ | @ 4 , | 2, 7 | 18, | e 16, | e 24, | e 22, | 18, | e 16, | e 18, | 16, | 18, | 16, / | Sequence 290, App | 27, | 1221, | e 272 | 23458 | 556, | w | 179 | 1, Ar | e 314 | 96, App | e 3430 | : 725, Ap | ce 3940, | : 30770, | 8979 | | 343, | 7241 | 12894, | о С | e 11 | 3, Ap | Sequence 13469, A |

ALIGNMENTS

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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/269,535 PRIOR FILING DATE: 2001-02-16
    0.00593
75.00
100.00%
                           Length:
Matches:
       Conservative:
1640
16
0
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US-09-954-456-554; Sequence 554, Application US/09954456; Patent No. US20020115057A1; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-93
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US-09-938-842A-93/c
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Query Match;
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                                                                                    APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
FILE OF INVENTION: Sets
FILE OF INVENTION: Sets
CURRENT EFFERICE: 689290-76
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR ETLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NIMBER OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                              PRIOR APPLICATION NUMBER: US/60/235,134 PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
APPLICATION NUMBER: US/60/235,637 FILING DATE: 2000-09-26
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Indels:
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Matches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30015, Application US/09864761 Patent No. US20020048763A1
                                                                                                                    PRIOR
PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
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NUMBER OF SEQ ID NOS: 2276
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OTHER INFORMATION: n=a
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                                                                                                                    APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                             FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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                                   APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                                                              FILING DATE: 2001-01-30
                                                                                               APPLICATION NUMBER: PCT/US01/00665
                   APPLICATION NUMBER: PCT/US01/00663
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FILING DATE:
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Hanzel, David K.
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Query Match:
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                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-X-1
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

OTHER INFORMATION: NT HIT: AB021490.2, EVALUE 7.40e-01

OTHER INFORMATION: EST_HUMAN HIT: BE612820.1, EVALUE 1.10e+00
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                                                                                                                                                                                          APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/180,312
                                                                                                       APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                   APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                FILING DATE: 2001-01-30
                                                                                  APPLICATION NUMBER: PCT/US01/0066
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                       FILING DATE:
                                       APPLICATION NUMBER: PCT/US01/00664
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Hanzel, David K.
NUMBER: PCT/US01/00669
                    2001-01-30
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Matches:
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US-10-026-188-3
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LENGTH: 597
TYPE: DNA
                                                                                                                           SOFTWARE: FastSEQ SEQ ID NO 3
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APPLICANT: Zuker, Charles S.
APPLICANT: Zhang, Yifeng
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                                                                                . TYPE: DNA
                                                                                                                                                                                                                                APPLICANT: The Regents of the University of California TITLE OF INVENTION: Assays for Taste Receptor Cell Spec TITLE OF INVENTION: Ion Channel FILE REFERENCE: 02307E-114910US CURRENT APPLICATION NUMBER: US/10/026,188 CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/259,379 PRIOR FILING DATE: 2000-12-29
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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FEATURE:
OTHER INFORMATION: MAP TO AL138761.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL =
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               OTHER INFORMATION: mouse genomic region containing ltrpc5
                                          FEATURE:
                                                        ORGANISM: Mus musculus
                                                                                                       LENGTH: 249487
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Alignment Scores: Pred. No.:

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Length:

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Best Local Similarity:
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NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11273
LENGTH: 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15
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                                                                                                                                                                                    LOCATION: (389)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
                                                                                                                                                                                                                                                        OCHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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                                       NAME/KEY: misc feature
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Best Local Similarity:
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                                                                  Sequence 865, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
                              APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For TITLE OF INVENTION: Expression
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Conservative:
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APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12894
LENGTH: 720
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: COTHER INFORMATION: n = A,T,C
US-10-198-846-12894
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Best Local Similarity:
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Query Match:
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RESULT 10
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CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-03-27
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
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TYPE: DNA.
ORGANISM: Bacillus licheniformis
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Best Local Similarity:
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                                                                                        Pred. No.:
                                                                                                            Alignment Scores
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                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 343
LENGTH: 5399
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 343, Application US/10225567A Dublication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
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SEQ ID NO 7241
LENGTH: 791
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Datasta
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APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, Ka
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NAME/KEY: misc_feature
LOCATION: 282, 300, 554, 592,
OTHER INFORMATION: n = A,T,C c
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Wang, Youzhen
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RESULT 14
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                                                                                                       US-10-075-846-4_COPY_192_207 (1-16) x US-09-764-891-8979 (1-10468)
                                                                                                                                                                 Query Match:
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US-09-764-891-8976
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Publication No. US2003007780881
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8979
LENGTH: 10468
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SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 8976
LENGTH: 10468
TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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; LOCATION: (1)...(263)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-30770
                                     Percent Similarity:
Best Local Similarity:
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GENERAL INFORMATION:
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SEQ ID NO 30770
LENGTH: 263
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LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30770, Application US/09918995
                                                                                                                                                                                                                                                                                                      APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/465,231
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR APPLICATION NUMBER: US 60/113,678
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
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| | Search completed: July 1, 2003, 01:01:55 Job time : 29.519 secs | US-10-075-846-4_COPY_192_207 (1-16) x US-09-983-965-3940 (1-381) Qy |
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Database : -Q-/G9n2_1/USPTO_spool/US10075846/runat_25062003_163648_5157/app_query.fasta_1.782
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-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: Searched: Scoring table: Sequence: Title: Perfect score: Run on: OM protein - nucleic search, using frame_plus_p2n model Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp June 30, 2003, 23:00:29 ; Search time 84.1163 Seconds (without alignments) 3080.588 Million cell updates/sec US-10-075-846-4_COPY_192_207 7: 9: 10: 11: 16154066 seqs, 8097743376 residues Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext BLOSUM62 113: 114: 115: 116: 117: 118: 119: 120: 221: 221: 223: 23: 24: SSSILCSPLPSLSLSV 16 em_estmu:*
em_estov:* gb_est1:* em_estro:* em_estpl: em_estin: * em_esthum:* em_estba:* em_gss_fun:* em_gss_vrt:* em_gss_pln: em_gss_hum:* em_gss_inv:* em_estfun:* gb_est4:* gb_htc:* gb_est2:* em_gss_other:* em_gss_mus:* em_gss_mam:* gb_gss:* em_estom:* gb_est5:* gb_est3:* em_gss_pro:* 0.5 0.5 7.0 32308132

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| G053401 Pan tro | 553 EST220 | Q193942 UI-R-C | 0785 | E117524 UI-R-BS1 | 1896388 fc80d10 | 06681 EST2349 | G380127 UI-R-CS | 388008 UI-R-C | 117765 UI-R-B | 44669 24424 | 46805 29517 MA | 2695 UI-R-CO- | 7038 ua39 | 5 60224763 | 1091085 60285528 | H501609 ВОНLC72 | 041152 Pan trog | 506723 1M0348F0 | 966794 2M0237 | F430050 256000 M | Z826665 2M0102F | 591971 hf36d1 | 449589 dae73b10 | 2713283 RPCI-24 | 64587 A065P41U | 346474 kx71e05. | G167249 60234 | Z198854 SP_1038_ | J237354 BJ23735 | J268516 BJ26851 | Q246138 TaE15015 | Q415379 RPCI-11 | V547337 AV54733 | V548438 AV54843 | V548451 AV548451 | E591974 WHE165 | V817296 AV817 | 597350 29621 1 | ES26547 M65F05ST | Z485951 1M0313 | G622007 60264660 | E739001 60155606 | 484167 pmp1c | 76357 Pan trog | Description | 2 |

ALIGNMENTS

| REFERENCE AUTHORS | | ORGANISM | | SOURCE | KEYWORDS | VERSION | ACCESSION | DEFINITION | LOCUS | AG076357/c | RESHLT 1 |
|--|---|-----------------|---------------------------------|---|----------|------------------------|------------|--|--|------------|----------|
| l Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. | Pan troglodytes | BAC Library clone:PTB-070I15.F. | Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male | GSS. | AG076357.1 GI:16628159 | AG076357 . | Pan troglodytes DNA, clone: PTB-070I15.F, genomic survey sequence. | AG076357 795 bp DNA linear GSS 03-NOV-2001 | | |

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BQ484167
BQ484167.1 GI:21328786
EST
Chicken.
                                                                                             University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-6473
Fax: 302-831-2822
                                                                                                                                                           Unpublished (2002)
Contact: Calvin Keeler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                              Gallus gallus
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          /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                             Location/Qualifiers
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nd Sakaki,Y.
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FEATURES
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BE739001/c
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Plate: LLCM492 row: f column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE739001 884
601556067F1 NIH_MGC_58 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BE739001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Cone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 16
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                                                                            /note="Organ: kidney; Fvector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATTGGCC-3' and 3' adaptor
sequence: 5'-CACGGCCAGCGCGCCAATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

23 a 208 c 280 g 173 t
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/sex="Male and Female"
/tissue_type="LPS-stimulated HD-11 macrophage cells"
/lab_host="E.coli xL-10 Blue"
/note="Vector: pBluescript II-SK"
119 c 56 g 60 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3825809"
/clone_lib="NIH_MGC_58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                        /tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be
                              SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSer 15
malia; Eutheria;
(bases 1 to 1081)
                                                                                                                                                                                                                                                                                527
                                                                                                                                                                                                                                                                                               /db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone="IMAGE:4768033"
/clone="IMAGE:4768033"
/clone="Ib="NIH_MGC_79"
/lab_host="DHIOB (Tl phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/note="Organ: placenta; Vector: pDNR-LIB (Glontech);
/site_1: Sfil (ggccstcggcc); Site_2: Sfil (ggccattatggcc); Site_2: And 3' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCCGGCCGACATG-dT(30)BN-3'
(where B = A, C, G or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
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Eutheria; Primates;
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                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0313 row: I column: 12
Seq primer: CACACAGGAAACAGCTATGACC
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84112,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ485951 128 bp DN AM2485951 128 bp DN AM2485951 128 MOUSE 10kb plasmid UUGCIM Clone UUGCIM0313112 R, DNA sequence. AZ485951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Wright,D.,Weiss,R. Mouse whole genome sca
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1 (bases 1 to 128)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                 (http://www.jax.crg/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gii4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and parafetred vector DNA and praced into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                           b
                                                                                                                                                                                    adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

14 g 43 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0313112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
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Rodentia;
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Query Match:

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                                                      DEFINITION
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1 (bases 1 to 263)

White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.

A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                       AA597350
29621 Lambda-PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clones were originally prepared at Michigan State University. Arabidopsis Biological Resource Center, The Ohio State University, 309 Botany & Zoology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 614292060 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email
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Fax: 517 353 9334
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Biochemistry & Molecular Biology
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Site_1: EcoRI; Site_2: XhoII"
38 c 79 g 61 t
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/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="600035219R1"
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s thaliana cDNA clone 196B17M4, mRNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; endicotyledons; Arabidopsis.
                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                     Arabidopsis thaliana
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Seg primer: 5' end dye terminator
Location/Qualifiers
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MSU-DOE Plant Research Laboratory
Michigan State University
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//Inote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
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/strain="var columbia"
/db_xref="taxon:3702"
/clone="196817M4"
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  Nakajima, M.,
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                             1 (bases 1 to 470)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Chao,S., Lazo,G.R., Malatrasi,M., Miller,R., P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R., P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Malatrasi,M., Miller,R., Paywen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. Nguyen,H.T., Heat stressed flag leaf cDNA library Unpublished (2000)
                                                                                                                                                                                                                                                                                                      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE591974 470 bp mRNA linear EST 18-AUG-20 WHE1651-1654_A09_A09ZS Wheat heat stressed flag leaf cDNA library Triticum aestivum cDNA clone WHE1651-1654_A09_A09, mRNA sequence.
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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Plant Functional Genomics Research Group
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Arakawa, T., Shil
and Shinozaki, K
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/lab_host="DHIOB"
/note="Site_1: BamHI; Site_2:
dehydration (1, 2, 5, 10, 24 hr) treatments"
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/db_xref="taxon:3702"
/clone="RAFL09-93-012"
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Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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1 (bases 1 to 547)
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AV548451 Arabidopsis
CDNA clone RZL54e05F
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                                                                                                                                                                 The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
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EST.
                                                                                                                                                                                                                                     Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                              A large scale analysis of cDNA in Arabidopsis thaliana: Generation
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                                                                                                                                 Yana 1532-3, Kisarazu, Chiba
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/dev_stage="Full tillering stage"
/lab_host="E coli SOLR"
/lab_host="E coli SOLR"
/lab_host="E coli SOLR"
/note="vector: Lambda Uni-ZAP XR, excised phagemid;
/note="vector: Lambda Uni-ZAP XR, excised phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give pBluescript phagemids in the Uni-ZAP XR, excised to give phagemids in the Uni-ZAP XR, excised to
                                                             asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
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/organism="Arabidopsis thaliana"
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A large scale analysis of cDNA in Arabidopsis thaliana: Generation
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/tlssue_type="roots"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI;
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/clone="RZL54c06F"
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/strain="Columbia"
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The First Laboratory for Plant
Kazusa DNA Research Institute
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Asamizu,E. and Tabata,S.
Asamizu,E. and Tabata,S.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 597)
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Email: asamizu@kazusa.or.jp,
Location/Qualifiers
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BQ246138
                       Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipey, MB, Canada R37 2M9
Tel: (204) 983-240
Email: scloutierem.agr.ca
was cloned directionally, not all sequences generated win primer were from the 5' end (same with forward primer and Average insert size is >1.4 kb
Plate: 015 row: F column: 10
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet os (info@resgen.com). BAC and search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_GSSs: RPCI-11-177K5.TV
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TaE15015F10R TaE15 Triticum aestivum cDNA clone TaE15015F10R, mRNA
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Class: BAC ends.
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Nector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Site_2: EcoRI;
/note="Nector: pBACe3.6; Site_2: EcoRI; EcoRI; Site_2: EcoRI; EcoRI
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/clone="RPCI-11-177K5"
/clone_lib="RPCI-11"
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/db_xref="GDB:7567828"
Location/Qualifiers
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1 (bases 1 to 615)
Ogihara, Y. and Murai, K.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BJ268516 1. Ogihara unpublished cDNA library, Wlassituum cDNA clone whoh17f17 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Tadasu Shin-i
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ВJ268516.1
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Location/Qualifiers
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown under hydroponic conditions at UC Davis, salt stressed for 12 hours, and for 7 days, then dissected and frozen (Akhunov in J Dvorak Lab). Total RNA was prepared from sheath tissue, equal quantities of RNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="15 days after anthesis"
/lab_host="E. coli DH108"
/note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies);
Site_1: NotI; Site_2: MluI; mRNA obtained from wheat se
of cultivar Glenlea 15 days post-anthesis"
a 126 c 183 g 106 t
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/clone="TaE15015F10R"
/clone_lib="TaE15"
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                                                                                                                                                                                                                                        /clone_lib="Y. Ogihara unpublished cDNA library, wh_oh"
/tissue_type="pistil at heading date"
/dev_stage="Feekes' scale 10.5"
                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whoh17f17"
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| performed in the OD Anderson lah (all other authors) " |
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| BASE COUNT 184 a 127 c 195 g 108 t 1 others |
| Alignment Scores: |
| Pred. No.: 1.38e+03 Length: 615 |
| Matches: |
| Percent Similarity: 75.00% Conservative: 1 |
| Best Local Similarity: 68.75% Mismatches: 4 |
| Query Match: 70.67% Indels: 0 |
| DB: 13 Gaps: 0 |
| US-10-075-846-4_COPY_192_207 (1-16) x BJ268516 (1-615) |
| Qy 1 SerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerVal 16 |
| Db 189 AGCAGCTCTTTCTGCTGTAGCCCCTCTCCCTGGTTTGAGCAGCAGCCTT 142 |
| Search completed: July 1, 2003, 00:55:32 |

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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ALIGNMENTS

AAG38474 RESULT 1

AAG38474 standard; Protein; 826 AA

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990S-0160814

990S-0160815

990S-0160815

990S-0160980

990S-0161980

990S-0161404

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990S-0161351

990S-0161352

990S-0161393

990S-0161993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   445
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  05-MAY 1999
06-MAY 1999
17-MAY 1999
11-MAY 1999
11-MAY
9908-0132485
9908-0132486
9908-0132863
9908-0134287
9908-0134218
9908-0134768
9908-0134770
9908-0135224
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9908-0143524
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9908-01444335
9908-0144884
9908-0144884
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99US-0145087. 99US-0145089. 99US-0145192. 99US-0145145. 99US-0145218.

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RESULT 3
AAG38472
ID AAG3
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Best Local S
Matches 11
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
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06-APR-1999
01-APR-1999
116-APR-1999
116-APR-1999
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29-OCT-1999
                                                                                                                                                                                                                                                                                                          Protein identification; sign; hybridisation assay; genetic termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                 AAG38472;
                                                                                                                                                                                                                                                                                                                                                                                                 AAG38472 standard;
                                                                                                                                                                                                                                      25-FEB-2000;
                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 47468
                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSSILCSPLPSLSLS
|||||| |:| |||||
| 460 SSSILMDPVPPLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 73.1
11; Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                      2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990S-0160770
990S-0160815
990S-0160980
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990S-0161404
990S-0161406
990S-0161350
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990S-0128274.
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990S-0139445.
990S-0130649.
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990S-0132484.
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73.3%;
                                                                                                                                                                                                                                                                                                                            signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                              474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 49; DB pred. No. 19; ly Mismatches
                                                                                                                                                                                                                                                                                                                   al transduction pathway; metabolic
mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                   AA
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promoter;
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22-JUL-1999
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20-AUG-1999
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20-AUG-1999
21-AUG-1999
21-AUG

99US-0145224.
99US-0145213.
99US-0145213.
99US-0145213.
99US-0145316.
99US-0146386.
99US-0146389.
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99US-0151086.

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| 022-AUG 03-AUG 03-AUG 04-AUG 05-AUG 06-AUG 06-AUG 07-AUG 0 | 27-JUL-199 27-JUL-199 27-JUL-199 27-JUL-199 28-JUL-199 |
| 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 06-AUG-1999 09-AUG-1999 11-AUG-1999 11-AUG | 27-JUL-1999; 9 27-JUL-1999; 9 27-JUL-1999; 9 28-JUL-1999; 9 28-JUL-1999; 9 |
| 02-AUG 1999 99UG 03-AUG 1999 99UG 04-AUG 1999 99UG 05-AUG 1999 99UG 06-AUG 1999 99UG 06-AUG 1999 99UG 10-AUG 1999 99UG 11-AUG 1999 99UG 11-AUG 1999 99UG 12-AUG 1999 99UG 12-AUG 1999 99UG 13-AUG 1999 99UG 14-AUG 1999 99UG 25-AUG 1999 99UG 26-AUG 1999 99UG 27-AUG 1999 99UG 27-AUG 1999 99UG 28-SEP 1999 99UG 29-SEP 1999 99UG 29-SEP 1999 99UG 29-SEP 1999 99UG 29-SEP 1999 99UG 21-OCT | 27-JUL-1999; 99US 27-JUL-1999; 99US 27-JUL-1999; 99US 28-JUL-1999; 99US 02-AUG-1999; 99US |
| 022 AUG -1999 03 AUG -1999 99US -011 04 AUG -1999 99US -011 05 AUG -1999 99US -011 06 AUG -1999 99US -011 07 AUG -1999 99US -011 08 AUG -1999 99US -011 11 AUG -1999 99US -011 12 AUG -1999 99US -011 13 AUG -1999 99US -011 14 AUG -1999 99US -011 15 AUG -1999 99US -011 16 AUG -1999 99US -011 17 AUG -1999 99US -011 18 AUG -1999 99US -011 19 AUG -1999 99US -011 10 AUG -1999 99US -011 11 AUG -1999 99US -011 12 AUG -1999 99US -011 13 AUG -1999 99US -011 14 AUG -1999 99US -011 15 SEP -1999 99US -011 16 SEP -1999 99US -011 17 AUG -1999 99US -011 18 AUG -1999 99US -011 19 AUG -1999 99US -011 10 AUG -1999 99US -011 11 AUG -1999 99US -011 12 AUG -1999 99US -011 13 AUG -1999 99US -011 14 AUG -1999 99US -011 15 AUG -1999 99US -011 16 AUG -1999 99US -011 17 AUG -1999 99US -011 18 AUG -1999 99US -011 19 AUG -1999 99US -011 11 AUG -1999 99US -011 11 AUG -1999 99US -011 12 AUG -1999 99US -011 13 AUG -1999 99US -011 14 AUG -1999 99US -011 15 AUG -1999 99US -011 16 AUG -1999 99US -011 17 AUG -1999 99US -011 18 AUG | 27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 27-JUL-1999; 99US-014 28-JUL-1999; 99US-014 28-JUL-1999; 99US-014 |
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Best Local S
Matches 11
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07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
 14-AUG-2000
22-AUG-2000
22-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200155320-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM94754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM94754 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        8-APR-2000;
9-MAY-2000;
7-JUN-2000;
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5-OCT-1999;

5-OCT-1999;

5-OCT-1999;

5-OCT-1999;

3-OCT-1999;

3-OCT-1999;

3-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SSSILCSPLPSLSLS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 73...
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2000US-0224519
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2000US-0225778
2000US-0225757
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2000US-0215135.
2000US-021647.
2000US-021680.
2000US-0217487.
2000US-0217496.
2000US-0217496.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0184664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161405.
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99US-0161350.
99US-0161361.
99US-0161361.
99US-0161902.
99US-0161992.
99US-0161992.
99US-0161993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 49; DB;
; Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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   22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

11-SEP-2000

11-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
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29-SEP
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2000US-0241785

2000US-0241786

2000US-0241787

2000US-0241809

2000US-0244819

2000US-0244617

2000US-0246474

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2000US-0246475

2000US-0246477

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2000US-0246477

2000US-0246477

2000US-0246523

2000US-0246525

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2000US-0246613
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2000US-0231242.
2000US-0231243.
2000US-0231244.
2000US-0231413.
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2000US-0229509.
2000US-0229513.
2000US-0230437.
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RESULT 5
AAB95892
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                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserv
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11-NOV-2000
01-DEC-2000
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08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                          Human; primer;
                                           Human protein sequence SEQ ID NO:19021.
                                                               26-JUN-2001
                                                                                AAB95892;
                                                                                                 AAB95892 standard; Protein; 160
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                        Claim 11;
                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                Rosen
                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC
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                                                                                                                                                          1 SSSILCSPLPSLSLS
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                                                                                                                                                SSSCLVSPLPSLFLA 80
                                                                                                                                                                                                                                                                                      SEQ ID NO 3412; 1297pp + Sequence Listing;
                                                                                                                                                                                                                         83 AA;
                                                                                                                                                                                                                                                                                                                                                                Barash
                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                    Conservative
                                                              (first entry)
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2000US-0251856.
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                         detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                            62.7%;
73.3%;
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3.5;
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29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                           the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cid sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 habbis and AAH13633 represent human amino acid sequences.
                                                                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                               of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5^{\prime}-end
                                                                                                                                                                                                                                                                                                                                                                                                                       to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                            Sequence
                                                                                                of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                    represent oligonucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID 19021;
                                                            160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0248036
62.7%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2537pp + CD ROM; English
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                                                                                                                       all of which are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S
A, Nagai K,
                    DB
                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K, Y
, Otsuki T;
                    Length 160;
                                                                                                                       the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto
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RESULT 6
ABB92207
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Query Match
Best Local S
Matches 8
                                                 31-MAY-2002
              Herbicidal; plant; agriculture; herbicide.
                              Herbicidally active polypeptide SEQ
                                                                                  ABB92207 standard; Protein;
                                                                                                                            55
                                                                                                                                            _
                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                            SSSILCSPLPSLSLS
                                                                                                                            TOKLLCSPLPHLAVS
                                                                                                                                                             Conservative
                                                (first entry)
                                                                                                                            69
                                                                                                                                             15
                                                                                  490
                                                                                                                                                            Score 47; DB Pred. No. 7; 4; Mismatches
                                ID NO 1418
                                                                                                                                                              0
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Best Local S
Matches 11
WPI; 2001-639362/73
N-PSDB; AAS88177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 1418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200210210-A2
                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                         30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tietjen K, Weidler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                  Novel human
                                                                                                                                                                                                                                                                                                                     ABG23990
                                                                                                                                                                                                                                                                                                                                           ABG23990 standard; Protein; 67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP09892
                                                            (HYSE-) HYSEQ INC
                                                                                                                                                   11-OCT-2001
                                                                                                                                                                                                                                                                                          18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                            210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSILCSPLPSLSLSV 16
                                                                                                                                                                                                                                                                                                                                                                                                          SSSLLSSPLPPPSLPV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490
                                                                                                                                                                                                                                                                 diagnostic protein #23981.
                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                    2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%;
68.8%;
                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 8
ABG11062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polypeptides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                             WPI; 2001-639362/73
                                                                                                                                            23-AUG-2000;
                                                                                                                                                            31-MAR-2000;
                                                                                                                                                                                          30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #11053
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG11062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG11062 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated
                                                                                                            (HYSE-)
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                        Human; chromosome
food supplement; m
                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 TSSFLCSPLP-LSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; SEQ ID No 54349; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SSSILCSPLPSLSL 14
                                                                              RT,
                              AAS75249
                                                                                                            HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                            Liu C,
                                                                                                                                            2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                      mapping; gene mapping; gene therapy;
medical imaging; diagnostic; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                          Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.7%;
78.6%;
                                                                               ΥŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
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s useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                         disorder
                                                                                                                                                                                                                                                                                                                                         forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
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New isolated polynucleotide and encoded polypeptides, useful

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RESULT 9
AAM23635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in generating antibodies against it, detecting or Guntitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                 25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                        Tang
                                                                                                                                                                                                                                                                                        tomato; monkey; dog; sea urchin; diagnostics; forensic test; gene biodiversity; gene therapy; nutr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                         25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                        02-AUG-2001.
                                                                                                                                                                                                                                    WO200154477-A2
                                                                                                                                                                                                                                                               Human herpesvirus
                                                                                                                                                                                                                                                                                                                                     Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                       HHV-2
                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM23635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide (II) sequences. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toca I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                        YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not appear in the fication, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                     EST encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSSILCSPLPSLSL
                        , Liu C, Z
Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSSFLCSPLP-LSL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID No 41421; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                 ; 2000US-0491404.
; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              relates to isolated polynucleotide (I) and II) sequences. (I) is useful as hybridisation probes.
                                        Zhou
                                                                                                                                                                                                                                                                                                                                                                    protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.7%;
78.6%;
                          Zhang
                                         ָש
                       Qian XB,
J, Werh
                                                                                                                                                                                                                                                                                             nutrition
                                                                                                                                                                                                                                                                                                         chin; expressed sequence tag; ES
gene mapping; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                    ID NO: 1160
                           Werhman
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                          Wang
man T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                        Asundi
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from WIPO
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RESULT 10
AAU14387
ID AAU14
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cow, pig, hamster, monkey, macaque, yeast, urchin and tomato. These were derived from from the organism of interest. They can be forensics, gene mapping, identification of biodiversity and for nutritional purposes. protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviantibacterial; antiallergic; dermatological; haemostatic; antiasthma
            proteins or their active domains. The polypeptides, polypucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as
                                                         The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins from a variety of organisms, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated po
antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH98294
                                                                                                                                 Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                       WO200155437-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human novel protein #258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU14387 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                  25-JAN-2000; 2000US-0491404
                                                                                                                                                                                                                                                                                                             25-JAN-2001; 2001WO-US02623
                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention provides the protein
                                                                                                                                                                                                                          YT,
                                                                                                                                                                                             2001-451939/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Page 850-851; 1275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                                                             AAS22692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCPPLPSLSCAI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCSPLPSLSLSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide for treatment of diseases, diagnostics, raising
                                                                                                    Page 795-796; 894pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                       C,
                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen; antibody; gene therapy; neurological disorder;
isease; inflammatory disorder; cancer; asthma; osteoporosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 immune disorder.
   food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45;
Pred. No.
supplements,
                                                                                                    English
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cluding human, dog, cat, horse, t, bacteria, fruit fly, sea the expressed sequence tags (ESTs) be used in diagnostics, of mutations, to assess s. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and coding sequences of novel
   in
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 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral;
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RESULT 11
AAY14488
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Best Local S
Matches 8
                                                                              Florence K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or from antiference resulting from bacterial, viral or from antiference resulting from bacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymu osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, the production of the invention can be used to target drugs to a tumour, in assays to determine biological activity, the production of the invention of the invention can be used to target drugs to a tumour, in assays to determine biological activity, the production of the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used as probes and primary for the invention are used to the invention can be used to the invention are used to
                        WPI; 1999-277587/23
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                                                                                                                                  Brewer LA,
                                                                                                                                                                                                                                                                                       09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9919339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fragment of human secreted protein encoded by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY14488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY14488 standard; Protein; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                  (HUMA-)
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                                                                                                                                                                                                  HUMAN GENOME
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8; Conser
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                                                                                 Yu G;
                                                                                                          Duan R,
, Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                        97US-0061529.
97US-0061532.
97US-0061536.
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97US-0061463.
97US-0061527.
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                                                                                                                                     Ebner
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                                                                                                          Olsen
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Pred:
                                                                                                                                        Ferrie AM,
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                                                                                                             ,SH
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                                                                                                             Rosen CA,
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15;
                                                                                                                                        Florence
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                                                                                                          SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoclast; thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 12
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Best Local :
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                                         07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                 04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the nucleic acid molecule detailed in the descriptor line. The can be used to generate fusion proteins by linking to the gene to human immunoglobulin Fc portion (e.g. AAX79002) for increasing the stability of the fused protein as compared to the human fine invention released protein as compared to the human fine fused protein as compared to the human fine invention released.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stability of the fused protein as compared to the human protein only. The invention relates to 53 novel genes and their fragments (nucleic acid sequences: AAX79011-X79064; amino acid sequences AAX74011-X14464) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 53 the conditions are the sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 53 the conditions are the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations in the sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by determining the presence of mutations are sample or by det
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive; antiinflammatory; anti-HIV; antibacteria;
antiparkinsonian; antisickling; antianaemic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
                                                                                                                                                                                                                     18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB17174 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides, based on which tissues they are most highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurological disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system related polypeptide SEQ ID NO
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8; Conser
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                  2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0205515
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                                                                                                                                                                    2000US-0214886
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2000US-0190076
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2000US-0186350.
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Pred. No.
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26-JUL-14-AUG-14-AUG-14-AUG-

2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213.

14 - AUG -14 - AUG -

2000US-0225266 2000US-0225267 2000US-0225268 2000US-0225270 2000US-0225270 2000US-0225757

2000US-0226681 2000US-0226868

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17-NOV-2000
The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
                                                                                                                                                                                                                                                                       WPI; 200
N-PSDB;
                                                                                                                                                                                           Claim
                                                                                                                                                                                                                               Nucleic acids encoding useful for preventing,
                                                                                                                                                                                                                                                                       2001-541565/60
)B; ABA13500.
                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                CA,
                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                         HUMAN GENOME
                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                               Barash
                                                                                                                                                                                                                    metastases
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2000US-024921
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2000US-024921
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2000US-0251130
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2000US-0254097.
2001US-0259678.
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2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
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2000US-0246632.

2000US-0246609.

2000US-0246610.

2000US-0246611.

2000US-0246613.

2000US-0249207.

2000US-0249207.

2000US-0249208.
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2000US-0246527
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2000US-0246477
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2000US-0251989
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2000US-0246525
                                                                                                                                                                                           ID NO
                                                                                                                                                                                                                                                                                                               SC,
                                                                                                                                                                                         5831;
                                                                                                                                                                                                                                                                                                                                         SCI INC
                                                                                                                                                                                                                       3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system
                                                                                                                                                                                        1701pp +
                                                                                                                                                                                                                                                                                                                , MS
                                                                                                                                                                                      Sequence Listing; English
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2000US-0231968. 2000US-0232397. 2000US-0230438. 2000US-0231242. 2000US-0231243. 2000US-0231244. 2000US-0231413.

2000US-0229509. 2000US-0229513. 2000US-0230437.

14 AUG 2000
15 AUG 2000
22 AUG 2000
23 AUG 2000
01 SEP 2000
01 SEP 2000
05 SEP 2000
06 SEP 2000
08 SEP 2000
08 SEP 2000
08 SEP 2000
09 SEP 2000
14 SEP 2000
14 SEP 2000
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18 SEP 2000
19 SEP 2000
10 SEP 2000
10 SEP 2000
10 SEP 2000
11 SEP 2000
12 SEP 2000
11 SEP 2000
12 SEP 2000
12 SEP 2000
13 OCT 2000
10 OCT 2000

2000US-0233063 2000US-0233064 2000US-0234223 2000US-0234274 2000US-023497 2000US-0234998 2000US-0234998 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0236370 2000US-0236370 2000US-0236370 2000US-0236370 2000US-0236370 2000US-0236370 2000US-0237038 2000US-0237038 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039

2000US-0240960 2000US-0241785 2000US-0241786 2000US-0241787 2000US-0241808 2000US-0241808 2000US-0241826 2000US-0241826 2000US-0246174 2000US-0246474 2000US-0246475

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RESULT 13
AAG00176
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 Query Match
Best Local S
Matches 9
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Best Local
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                                                                                                                             The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' conds and can therefore by used to other isolating cDNA sequences form mRNAs with intact 5' conds and can therefore by used to other full locations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; and (f) infectious diseases such as viral, bacteria and parasitic infections.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                       Sequence
                                                                                                                    ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                                                                                                  Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                          chromosome mapping
                                                                                                                                                                                                                                                                                           diagnostic,
                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC00182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG00176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG00176 standard; Protein; 149
                                                                              regulatory
                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1999;
 Local Similarity hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                           2000-500381/45.
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                                                                          ESTs are also used in diagnostic, forensic, gene therapome mapping procedures. They are used to obtain upstream ory sequences and to design expression and secretion vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST;
                                                                                                                                                                                                                                                               SEQ ID 4257; 71pp + CD-ROM; English
                                                       149
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  Conservative
                                                                                                                                                                                                                                                                                           forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome mapping.
                                                     A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    Ū,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
            58.7%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
58
                                                                                                                                                                                                                                                                                         gene therapy and chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tag;
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             Score
Pred.
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Pred.
  Mismatches
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A
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            No .
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16;
             DB
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein;
                          21;
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2;
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                          Length 149;
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                                                                                                                                                                                                                                                                                         mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                       gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     part of the format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA isolation;
0;
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                                                                              vectors
Gaps
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0;
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RESULT 14
AAM39431
ID AAM39
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25-APR-2000;
09-JUL-2000;
                                                          Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                   in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                 Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Sequence
                                    C.N.S disorders
Note: The seque
                                                                                                                                                                                                                                                           Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                     Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM39431 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukaemia.
                                                                                                                                                                                                                                                                                                                                  J,
QA,
                                                                                                                                                                                                                                                                                                           2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide
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                                                                                                                                                                                                                                                                                                 AAI58587
                                                                                                                                                                                                                                                                                                                                  , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSQIITSPLPSVS
                                     sequence data
 887
                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0488725.

2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0620312.

2000US-0653450.

2000US-0662191.

2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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 AA;
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                  2576; 10078pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                           polypeptides, useful
system injuries -
                                    for this patent did
                                                                                                                                                                                                                                                                                                                                              Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2576
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Xue AJ,
                                                                                                                                                                                                                                   English.
                                     not
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                                                                                                                                                                                                                                                                                                                                              Qian X
Yang
                                     form
                                                                                                                                                                                                                                                                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                               g Y,
                                    part of
                                                                                                                                                                                                                                                                                                                                              Zhang
                                                                                                                                                                                                                                                                                                                                                          Ren
                                                                                                                                                                                                                                                                        disorders
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(1)
                                    the printed
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CNS;
                                                                                                                                                                                                                                                                                                                                                          Wang
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Query Match

58

. 78;

Score

44;

DB 22;

Length 887

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RESULT 15
AAM39109
В
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25-JAP-2000; 2000US-0552317;
09-JUL-2000; 2000US-0598042;
19-JUL-2000; 2000US-0620312;
03-AUG-2000; 2000US-0652191;
14-SEP-2000; 2000US-0662191;
19-OCT-2000; 2000US-0693036
                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; centrial nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 2254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM39109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM39109 standard; Protein; 274 AA
                      assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 2254; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2000; 2000WO-US34263
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            specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-2000;
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DB; AAI58265.
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Wang Z,
Zhou P,
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Wehrman T, X
, Goodrich R,
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, Xu C,
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                                                                                                                                                                                                                                                                                                                                                                                             hen R, Ma Y,
Xu C, Xue AJ,
Drmanac RT;
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Yang Y,
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Zhang J;
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145 SPSLLQCPLPSLSL 158
                                  10;
         1 SSSILCSPLPSLSL 14
                                                                   274 AA;
                                  Conservative
                                          57.3%;
71.4%;
                                          Score 43;
Pred. No.
                                  Mismatches
                                        DB 54;
                                                  22; Length 274;
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                                  Indels
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                                 Gaps
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Search completed: June 25, 2003, 17:15:33 Job time: 3.32662 secs

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Title:

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Result
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Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-177-249-208
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US-09-177-249-208
US-09-178-184-2
US-09-28-18114-13
PCT-US95-11114-13
PCT-US95-11114-13
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PCS-08-485-607-88-124
PCS-08-485-124
PCS-09-137-721A-4
PCS-09-137-721A-4
PCS-09-137-721A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
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| 36 48.0 896 4 US-08-618-957A-10 36 48.0 898 2 US-08-693-697-36 36 48.0 898 4 US-08-618-957A-10 36 48.0 906 2 US-08-618-957A-9 36 48.0 906 2 US-08-618-957A-9 36 48.0 908 2 US-08-618-957A-9 36 48.0 908 2 US-08-618-957A-9 36 48.0 998 2 US-08-618-957A-8 36 48.0 958 2 US-08-618-957A-8 36 48.0 958 2 US-08-618-957A-8 36 48.0 950 1 US-08-918-919-3 36 48.0 960 2 US-08-918-191-3 36 48.0 960 2 US-08-93-697-8 36 48.0 960 3 US-08-693-697-8 36 48.0 960 3 US-08-618-957A-3 36 48.0 960 3 US-08-693-697-8 |
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/288,143
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: GO/061,463
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
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EARLIER APPLICATION NUMBER: 60/061,536
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EARLIER APPLICATION NUMBER: 60/061,532
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EARLIER FILING DA
                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-177-249-208
                             Sequence 208, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
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15 TSQLCSPMPSLN 26
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8; Conserv
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66.7%;
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Pred. No.
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APPLICANT: Margossian, Linda APPLICANT: Harada, John

PPLICANT: Goldberg,

Robert B.

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Query Match
Best Local Similarity
""" 6 8; Conserva
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NUMBER OF SEQ ID NOS: 324
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 208
LENGTH: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/177, 249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
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                                                       NFORMATION FOR SEQ ID NO:
                                                                                        NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: M0656/7036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051,753
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,919
FILING DATE: 12-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baltimore, David
TITLE OF INVENTION: DAXX, A NOVEL FAS-BINDING
TITLE OF INVENTION: PROTEIN THAT ACTIVATES JNK AND APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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 TYPE: 6
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
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                                                                           617-720-2441
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72.7%;
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Pred. No. 7
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Best Local Similarity
Watches 9; Conserve
                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6287786 1772859CD1
US-09-629-774A-2
                                                                                                                              ; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09629774A Patent No: 6287786
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                                                                                                                                                                                                                                                   APPLICANT: Kaser, Matthew R.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: PHOSPHOLIPID TRANSFER PROTEIN
FILE REFERENCE: PC-0003-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/328,869B
CURRENT FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 17
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APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: PHOSPHOLIPID TRANSFER PROTEIN
FILE REFERENCE: PC-0003 US
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/629,774A
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens FEATURE: -
                                                                                                                    FEATURE:
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TOPOLOGY: lin
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               Conservative
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88.9%;
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69.2%;
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                           Score 39; DB
Pred. No. 95;
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Pred. No.
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Pred. No.
                 Mismatches
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US-08-299-187-13
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                                                                                  RESULT 7
PCT-US95-11114-13
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TELEX: 133521
INFORMATION FOR SEO ID NO: 13
SEQUENCE CHARACTERISTICS:
FRIGTH: 13 amino acids
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                                                        Sequence 13, Application PC/TUS9511114 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                Matches
APPLICANT: APPLICANT:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Park, David
APPLICANT: Ricketts, Michael H.
                              APPLICANT:
                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
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ANTI-SENSE:
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TELEPHONE: 201 487-5800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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6; Conserv
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               Manowitz, Paul
Poretz, Ronald D.
Park, David
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Pred. No. 4.6;
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US-07-956-700B-84
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                                                                                                                                                  Sequence 84, Application US/07956700B Patent No. 5539092
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APPLICANT: Robert
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                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE: ORGANISM: Hom
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SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                      TITLE OF INVENTION: Cy
TITLE OF INVENTION: Ca
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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STATE: New Jerse
                             STREET:
                                         ADDRESSEE:
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CLASSIFICATION:
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FILING DATE: 21-JUN-1995
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Chicago
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                         E: Arnold, White & Durkee
321 No. 5539092th Clark Street
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411 Hackensack Avenue
                                                                                                       Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-CoA
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COUNTRY:

60610

Floppy Disk

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Query Match
Best Local Similarity
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US-08-476-537-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
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TELEFAX: 1-312-755-44
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INFORMATION FOR SEQ ID NO: 84:
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MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5756290th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                               TELEPHONE:
                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                          SOFTWARE: ASCII-DOS
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Amino acid
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                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert Haselkorn and Piotr Gornicki
RVENTION: Cyanobacterial and Plant Acetyl-Coa
RVENTION: Carboxylase
               1-312-755-4489
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                               1-312-744-0090
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Pred. No.
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RESULT 11 US-08-475-879-84

; Sequence 84, Application US/08475879
; Patent No. 5972644

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STRANDEDNESS:
TOPOLOGY: Lin
MOLECULE TYPE:
US-08-476-537-84
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Best Local Similarity
"hehes 7; Conserve
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                                                                                                               ; MOLECULE TYPE: US-08-485-607-84
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                                                        Matches
                                                                       Best
                                                                                   Query Match
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APPLICANT: Robert
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 1-312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: STREET: Chicago
                                                        Local Similarity hes 7; Conserv
                                                                                                                                          STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 251 ....
                                                                                                                                                                                                                                                                                      NAME: Thomas E. No. 5792627thrup REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                  LENGTH:
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181 TSSVLRSPMPGVVVAV 196
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                            1 SSSILCSPLPSLSLSV 16
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321 No. 5792627th Clark Street
                                                                                                                                                                                                                               1-312-755-4489
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                                                        Conservative
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                                                                                                                             Peptide
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43.8%;
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Pred. No. 1.1e+02;
                                                                      Score 38;
Pred. No.
                                                        Mismatches
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                                                                      1.1e+02;
                                                                                    DB 1;
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                                                                                   Length 251;
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                                                       Indels
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Patent No. 5972644 5786170

GENERAL INFORMATION:

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                                                       SEQ ID NO 84
LENGTH: 251
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                             sequence 84, Application US/09433043B
Patent No. 6399342
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                                                                                                                                                                              FILE REFERENCE: ARCD:338US
CURRENT APPLICATION NUMBER: US/09/433,043B
CURRENT FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/475,879
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                     APPLICANT: HASELKORN, ROBERT
APPLICANT: GORNICKI, PIOTR
TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
                                                                                                            NUMBER OF SEQ ID NOS: 1:
SOFTWARE: PatentIn Ver.
                                                                                                                                                PRIOR APPLICATION NUMBER: 07/956,700 PRIOR FILING DATE: 1992-10-02
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                                  ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence:
                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5972644 5786170th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: LI
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino acids
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STATE: Illinois
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IVENTION: Cyanobacterial and Plant Acetyl-Coa
IVENTION: Carboxylase
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Linear
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1.1e+02
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Synthetic
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Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                  ; MOLECULE TYPE: protein US-08-476-008-50
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Patent No. 5627061
                                   Matches
                                                 Query Match
Best Local
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION UNMBER: US 07/749,611
FILING DATE: 28-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsa STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 31-AUG-1990 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                   LENGTH:
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1 SSSILCSPLPSLSLS 15
                                    Similarity 7; Conser
                                                                                                                                                 amino acids
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                                                                                                                                                                                                                        (314)537-6047
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                                 50.7%; Score 38; DB 1; llarity 46.7%; Pred. No. 2.2e+02; Conservative 5; Mismatches 3
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43.8%;
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Pred. No.
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                                                                Length 460;
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US-08-306-063-50
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                                                                                                                         Sequence 50, App...
Sequence 50, App...
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                              GENERAL INFORMATION:
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APPLICANT: Barry, Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            APPLICANT: Stalling TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION.
PRIOR APPLICATION DATA:
US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                 APPLICANT:
                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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NUMBER
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                                                                                                                                                                                                                                                                                                  Local Similarity 46.
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 31-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/306,063 FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  460 amino acids
          Barry, Gerard F.
Kishbore, Ganesh M.
Padgette, Stephen R.
Stallings, William C.
SVENTION: Glyphosate Tolerant
VENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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Kishore, Ganesh M.
Padgette, Stephen R.
Stallings, William C
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Pred. No. 2.
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Best Local Similarity
Trhas 7; Conserv
 Job time :
               Search completed: June 25, 2003, 17:18:07
                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-833-485-50
                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 13-SEP-
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                       LENGTH: 460 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0'
FILING DATE: 31-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                       (314)737-6047
                                                                                                                             Conservative
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46.78;
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Pred. No.
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                                                                                                                             Mismatches
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Minimum DB seq
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptcdata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

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7: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09_NEW_PUB.pep:*

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10: /cgn2_6/ptcdata/1/pubpaa/US10_NEW_PUB.pep:*

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      US-10-075-846-4_COPY_192_207
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 US-10-075-846-74
US-10-075-846-15
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US-09-775-846-91
US-09-771-151A-102
US-09-771-151A-193
US-09-771-153-208
US-09-771-155-49
US-09-747-155-49
US-09-746-2844-23
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1307.255 Million cell updates/sec
Sequence 74, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 205, App
Sequence 102, App
Sequence 101, App
Sequence 102, App
Sequence 103, App
Sequence 208, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 86, Appl
Sequence 86, Appl
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US-10-075-846-74
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 37.5 | 37.5 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 39 |
| 50.0 | 50.0 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 50.7 | 52.0 | 52.0 | 52.0 | 52.0 | 52.0 | 52.0 | 52.0 | 52.0 |
| 300 | 126 | 943 | 943 | 897 | 827 | 667 | 621 | 491 | 460 | 460 | 362 | 346 | 141 | 105 | 76 | 41 | 25 | 359 | 351 | 347 | . 270 | 218 | 178 | 123 | 68 |
| 9 | 10 | 9 | 9 | 9 | 9 | 10 | 10 | 9 | 10 | 9 | 9 | 9 | 10 | 10 | 9 | 10 | 10 | 9 | 9 | 10 | 10 | 9 | 10 | 9 | 9 |
| US-10-174-590-548 | US-09-740-668A-42 | US-10-256-702-7 | US-09-933-261-7 | US-10-138-927-45 | US-10-101-464A-915 | US-09-816-127-1 | US-09-733-300-4 | US-09-965-529-12 | US-09-861-696-50 | US-09-464-099A-50 | US-09-796-753-142 | US-10-085-108-22 | US-09-864-761-37903 | US-09-739-907-157 | US-10-106-698-5785 | US-09-864-761-47002 | US-09-864-761-36023 | US-10-205-823-60 | US-10-106-698-4697 | US-09-925-301-985 | US-09-841-132-404 | US-09-764-891-3995 | US-09-811-284-256 | US-09-764-891-2743 | US-10-106-698-5490 |
| Sequence 548, App | Sequence 42, Appl | Sequence 7, Appli | Sequence 7, Appli | Sequence 45, Appl | Sequence 915, App | Sequence 1, Appli | 4 | Sequence 12, Appl | Sequence 50, Appl | Sequence 50, Appl | Sequence 142, App | Sequence 22, Appl | Sequence 37903, A | Sequence 157, App | Sequence 5785, Ap | Sequence 47002, A | Sequence 36023, A | Sequence 60, Appl | Sequence 4697, Ap | Sequence 985, App | Sequence 404, App | Sequence 3995, Ap | Sequence 256, App | Sequence 2743, Ap | Sequence 5490, Ap |

ALIGNMENTS

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RESULT 2
US-10-075-846-15
; Sequence 15, Application US/10075846
; Publication No. US20030032608A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
; TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
; FILE REFERENCE: D0079 NP
; CURRENT APPLICATION NUMBER: US/10/075,846
; CURRENT FILING DATE: 2007-02-13
; PRIOR APPLICATION NUMBER: US 60/269,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Homo sapiens US-10-075-846-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 81
SOFTWARE: Patentin version 3.0
SEO ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
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Pred. No.
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; NAME/KEY: SITE ; LOCATION: (51) ; LOCATION: (51) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3412
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; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-075-846-4
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                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3412
LENGTH: 83
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Sequence 3412, Application US/09764891 Publication No. US20030077808A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYMUCLECTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT :
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREO;
FILE REFERENCE: D0079 NP
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                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                           TYPE: PRT
                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 SSSILCSPLPSLSLSV 207
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73.3%;
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Pred. No.
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       No.
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US-09-771-161A-102
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; ORGANISM: Homo sapiens
US-10-150-111-205
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; ORGANISM: Homo sapiens
US-09-771-161A-102
                                                                     SOFTWARE: PatentIn version 3.0 SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/09771161A Patent No. US20020110811A1
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                                                                                                        PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/724,676
PRIOR TILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 802620-2005.1
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CURRENT FILING DATE: 2002-05-20
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PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/288,143 PRIOR FILING DATE: 1999-04-08
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                                        TYPE: PRT
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FILING DATE: 1998-10-08
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5. US20030078386A1
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Pred. No. 7
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US-09-771-161A-101
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                                                                                                                  ; ORGANISM: Homo sapiens US-09-771-161A-192
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US-09-771-161A-192
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PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
                                                Query Match
Best Local S
Matches 9
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SEQ ID NO 192
LENGTH: 887
TYPE: PRT
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APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
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LENGTH: 756
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Best Local (
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
CURRENT FILING DATE: 00.773.676
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PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
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PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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                                                y Match 58.7%;
Local Similarity 69.2%;
hes 9; Conservative
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69.2%;
                                                Score 44; DB Pred. No. 94; 2; Mismatches
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Pred. No. 54;
2; Mismatches
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Pred. No. 80;
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                                                                DB 10; Length 887; 94;
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RESULT 9
US-09-771-161A-193
; Sequence 193, App
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Best Local Similarity
Gatches 9; Conserva
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TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILLE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-12
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Best Local S
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SEQ ID NO 208
LENGTH: 106
TYPE: PRT
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                                                                                                                                                                                                                                                                                               APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
FILE REFERENCE: 023070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
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4 ILCSPLPSLSL 14
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o. US20030110536A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robert L.
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69.2%;
                                                                       57.3%;
72.7%;

    Mismatches

                                                                       Score 43; DB Pred. No. 16;
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Pred. No.
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61 MLCSPFPSLHL 71

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Query Match
Best Local Similarity
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US-10-150-821-4
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                               Sequence 4, Application US/10150821
Publication No. US20020192758A1
GENERAL INFORMATION:
APPLICANT: Welcher, Amdrew A.
APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C38/C48 COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/10/150,821
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: US/09/911,842
PRIOR FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-07-24
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     PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300
NFORMATION FOR SEQ ID NO: 208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BASTLAN, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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   APPLICATION FILING DATE:
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California
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Yadegari, Ramin
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N: 800
NUMBER: US 60/222,438: 2000-08-01
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72.7%;
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Pred. No.
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NAME/KEY: misc_feature

; LOCATION: (1757)..()

; OTHER INFORMATION: Xaa = any or unknown amino acid

US-10-150-821-4
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US-09-747-155-49
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LENGTH: 3594
TYPE: PRT
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Best Local S
Matches 10
                                                                                                                                     Sequence 49, Application US/09747155
Patent No. US20020151692A1
GENERAL INFORMATION:
APPLICANT: Rouquier, Sylvie
APPLICANT: Giorgi, Dominique
TITLE OF INVENTION: No. US20020151692A1el Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 19904-008 (C00986334US)
SOFTWARE: PatentIn version 3.0 SEQ ID NO 49 LENGTH: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
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                                                                      CURRENT APPLICATION NUMBER: US/09/747,155
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/171,746
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Elliott, Gary S.
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF FILE REFERENCE: 01017/37592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Welcher, Amdrew A.
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                                                     NUMBER OF SEQ ID NOS: 431
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Sequence 196, Application US/10001857
Publication No. US20020183500A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0273
CURRENT FILING DATE: US/10/001,857
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,054
PRIOR FILING DATE: 2000-11-20
INMBER OF SEQ ID NOS: 208
SOPTWARE: Patentin version 3.1
SEQ ID NO 196
LENGTH: 310
TYPE: PRT
ORGANISM: Homo sapien
Search completed: June 25, 2003, 17:18:51 Job time: 2.32438 secs
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US-10-001-857-196
                                                                                                                                                                          Query Match 54.7%; Score 41; DB 9; Length 310; Best Local Similarity 66.7%; Pred. No. 94; Matches 10; Conservative 1; Mismatches 4; Indels
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| 125 SHSLLCVLPPSLSLS 139
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| Score 46; DB 2; Length Pred. No. 2.2; 4; Mismatches 3; Ind | [imported] - Escherich ision 16-Feb-2001 #text Burland, V.; Mau, B.; G. N.W.; Lim, A.; Dimalan ohemorrhagic Escherichi 21074935; PMID:11206551 21074935; PMID:11206551 21074935; PMID:11206551 | Score 49; DB 2; Len Pred. No. 2.9; 1; Mismatches 3; | Arabidopsis thalian mouse-ear cress) ision 02-Jun-2000 # ttet, A.; Mache, R. Database, April 20 [SSPDB:GN00061; AT olumbia; BAC clone] | ALIGNMENTS | A54773 A85093 F71555 T10677 G86736 A82538 A727206 T49541 T30889 T36089 B85069 B85069 B85069 T46915 T11046 S277752 |
| gth 117; Indels 0; Gaps 0; | ia coli (strain O157:H7, subs _change 14-Sep-2001 lasner, J.D.; Rose, D.J.; May ta, E.; Potamousis, K.; Apoda a coli O157:H7. | gth 490; Indels 0; Gaps 0; | a text_change 02-Jun-2000 ; Mewes, H.W.; Rudd, S.; Lemcke, 00 SP:F4F15.280 F4F15 | | Acl protein - mous hypothetical prote pathogenesis-relat hypothetical prote pathogenesis-relat hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable lacr-fami hypothetical prote probable lacr-fami hypothetical prote amino acid permeas NADH2 dehydrogenas anthranilate synth anthranilate synth |

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A:Map position: segment S
C:Superfamily: bunyavirus nonstructural protein
C:Keywords: nonstructural protein
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                   R; Kawarabayasi, Y.; Hino, Y.; Jawa, H.; Takamiya, M.; Masuda, Bana Res. 6, 83-101, 1999
                                                                             hypothetical protein APE1566 - Aeropyrum pernix (strain K1) c;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch C;Accession: A72535
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A;Title: A human phosphatidylinositol 3-kinase complex related A;Reference number: S57219; MUID:95354652; PMID:7628435
A;Accession: S57219
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A; Residues: 1-91 < AKA>
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Virus Res. 1, 51-63, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S07943
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A; Residues: 1-887 < VOL>
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                                        S.; Funahashi, T.; Tanaka, T.;
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     aerobic
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                               Yamazaki, S.; Haikawa, Y.; Jin-no, n.,
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 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
                                                      probable polynucleotide adenylyltransferase (pcnA) - syphilis spirochete C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-19 C;Accession: H71345 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; I
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; Weidman, J.,
281, 375-388,
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Roliveira, R.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Feference, P. M. Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Peference, P. M. Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Peference, P. M. Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Peference, P. M. Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Peference, P. M. Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., N. Peference, P. M. Peferen
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A:Title: The genome sequence of the plant pathogen Xylella fastidiosa A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 be
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A; Residues: 1-114 <KAW>
A; Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80566.1; PID:d1044352; PID:g
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Chidambaram,

G.G.; Dodson, Utterback,

7 R

spirochete)
- change 05-Nov-1999

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A; Cross-references: EMBL:AC004680; NID:g3420043; PID:g3420049
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; Vanhken, S.E.; Umayam, L.; Taleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84703
                                                                                                                                                                                                                                                                    A.Reference number: 214675
A.Recession: T02483
A.Recession: T02483
A.Recession: T02483
                                                                                                                                                                                                                                                                                                                                                                        probable protein phosphatase 2C At2g30020 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F23F1.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 03-Jun-2002
C;Accession: T02483; E84703
C;R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
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A; Residues: 1-478 <COL>
A; Cross-references: GB: AE001208; GB: AE000520; NID: g3322538; PIDN: AAC65258.1; A: Experimental source: strain Nichols
                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-396 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1010 <MCD>
A;Residues: 1-1010 <MCD>
A;Cross-references: EMBL:AL109957; PIDN:CAB53076.1; GSPDB:GN00068; SPDB:SPCC16A11.04
A;Experimental source: strain 972h-; cosmid c16A11
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A;Reference number: Z21822
A;Accession: T41077
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I Similarity 62.5%;
10; Conservative
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nilarity 53.8%;
Conservative
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Pred. No.
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Pred. No.
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                                                                                                                  Town, C.D.; Fujii, C.Y
E.; Umayam, L.; Tallon,
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lon, L.
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wi
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408; 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mail
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mail
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Ser, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Pitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis
A;Reference number: A86141; MUID:21016719; PMID:11130712
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T38130
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A:Map position: 2
A:Introns: 168/3
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
                                                                   A; Molecule type: DNA
A; Residues: 1-2123 <
                                                                                                       A. Status: preliminary
                                                                                                                              A; Reference number: A86141; A; Accession: F86348
                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: F86348
                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F24J8.17 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A; Residues: 1-396 <S
A; Map
                                          A;Cross-references: GB:AE005172; NID:g9454580; PIDN:AAF87903.1; GSPDB:GN00141
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66.78;
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Pred. No.
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1.1e+02;
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47;
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Maiti, R.; Marzia
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Query Match

54.7%;

Score

41;

BB

2

Length 2123

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RESULT 13
D71557
                               hypothetical protein F19C14.10 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96616
                                                                                        RESULT
D96616
                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A71570; MUID:99000809; PMID:9784136
                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein CT109 - Chlamydia trachomatis (serotype D, strain UW3/Cx) C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 C;Accession: D71557
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T22881
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   R; Theologis, Chin, C.W.;
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                                                                                                                                                                                                                                                                                 A; Experimental source: serotype D, C; Genetics:
                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001284; GB:AE001273; NID:g3328494; PIDN:AAC67700.1; A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                               R; Stephens, R.S.; Kalman, Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 106/3
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A; Map position: 2
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A;Experimental source: clone F57G9
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A; Residues: 1-247 <WIL>
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Gene: CT109
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Chung, M.K.;
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                J.R.;
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77.8%;
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               Palm,
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Conway, A.B.; Conv
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                Kaul,
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 Creasy, T.H.;
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 Dewar,
               Alonso,
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Search completed: June 25, 2003, 17:17:36 Job time: 3.07383 secs

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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Maiti, Rizco, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                           A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35338.1; PID:e27303; A;Note: this sequence was submitted to the EMBL Data Library, December 19; A;Note: this reading frame extends between two stop codons and does not be
                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-798 <CHE>
                                                                                                                                                                                                                                                                                                              Curr. Top. Microbiol. Immunol. 154, 125-169, 1990 A;Title: Analysis of the protein-coding content of the sequence of A;Reference number: S09749; MUID:90269039; PMID:2161319 A;Accession: S09867
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Note: host Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: S09867
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S09867
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A;Molecule type: DNA
A;Residues: 1-313 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                        R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, M.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein UL102 - human cytomegalovirus C;Species: human cytomegalovirus, human herpesvirus
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human herpesvirus 5
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                      Score
 39
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Gapop 10.0 ,
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SwissProt_40:*
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Listing first 45 summaries
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EFTU_ARATH
FIG2_YEAST
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TRPX_ARATH
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A4B1_MOUSE
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VG27_HSVI1
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P11970
083108
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P16954
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Q44239
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P32237
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P53907
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P16827
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Q95247 sus scrofa
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| This SWISS-PROT entr between the Swiss I the European Bioinfo use by non-profit modified and this st entities requires a or send an email to | SEQUENCE F MEDLINE-85 Akashi H., Localized bunyavirus Aino virus Virus Res!- SIMILA AND TO | L_AINOV STANDA P12413; 01-OCT-1989 (Rel. 12, 01-JAN-1990 (Rel. 12, 01-JAN-1990 (Rel. 13, Nonstructural protein Aino virus Viruses; ssrNA negati NCBI TaxID-11582; | 34 335 336 338 338 338 442 442 443 |
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Query Match Best Local S Matches 8 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence up 01-JAN-1990 (Rel. 13, Last annotation Nonstructural protein NS-S. Aino virus. Virus. This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial SEQUENCE FROM N.A. MEDLINE-#85170502; PubMed=#6532000; Akashi H., Gay M., Thara T., Bishop D.H.L.; Akashi H., Gay M., Thara T., Bishop D.H.L.; *Localized conserved regions of the S RNA gene products of bunyaviruses are revealed by sequence analyses of the Simbu serogr bunyaviruses are revealed by sequence analyses of the Simbu serogr Virus Res. 1:51-63(1984). -j. SIMILARITY: 35% TO LA CROSSE BUNYAVIRUS NONSTRUCTURAL PROTEIN AND TO SNOWSHOE HARE BUNYAVIRUS NS-S. InterPro; IPR000797; Bunya_NSs. Infam; pF01104; Bunya_NS-S; 1 ProDom; PD002170; Bunya_NS-S; 1. EMBL; M22011; AAA42544.1; -. PIR; S07943; MNVUAV entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Viruses; ssRNA negative-strand NCBI_TaxID=11582; Nonstructural SEQUENCE 91 73 1 SSSILCSPLPSLSL 14 Similarity 57.1 8; Conservative TOQILCOTLPSLSI 86 protein. AA; 10503 MW; 56.0%; 57.1%; Score 42; D Pred. No. 1. 2; Mismatche 6B91955505744BA0 CRC64; viruses; Bunyaviridae; Orthobunyavirus Mismatches update) update) DB 1; Length 91; products of of the Simbu serogroup Indels 0 collaboration 0

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OPRM_PIG STANDARD: PRT; 401 AA. 095247; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 0PRM1.

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"The porcine mu opioid receptor: molecular cloning and mRNA distribution in lymphoid tissues.";
J. Neuroimmunol. 90:192-198(1998).
-I-FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING ON CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. REPOR BETA-ENDORPHIN.
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PRINTS; PR00237; GPCRRHODDPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.
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Mammalia; Euther
NCBI_TaxID-9823;
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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p31170;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Small heat shock protein, chloroplast precursor.
HSP21 OR AT4G27670 OR T29A15.160.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnollophyta; eudicottyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                           MEDLINE=91360086; PubMed=1886617;
Chen Q., Vierling E.;
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Viruses; dsDNA viruses, no RNA
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                                                                                                                                                                        "Analysis of conserved domains identifies
                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                         chloroplast heat shock protein."; Gen. Genet. 226:425-431(1991).
                                                                                                                                                                                      Q., Vierling E.
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9; Conserv
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
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RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Lark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Dose S., de Haan M., Marse A.C., Schaefer M., Mueller-Auer S.,
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RA Glabon T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
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RA Perez Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Kohes M., Abu-Threideb J.,
RA Arnenil L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnabl S., Falten M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideb J., Stocket S.,
RA Kamer J., Fulton L., Mardis E., Dante M., Pepin K., Johnson D.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Johnson D.,
RA Kramer J., Fulton S., Mahaman D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Bershoff A., Jones K., Drone K., Cotton M., Joshu C.,
RA Martis M., Martiensen R., McCombie M., R.,
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Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R.,
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                                                                                                                                                                European Bioinformatics Institute.
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A) tail length of a heat shock protein RNA is increased
heat stress, but intron splicing is unaffected.";
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Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
S.-A., McCulladh B. Bilham
                                                                            d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                           as its content
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                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller M.,
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                                                                                                                                                                                         a collaboration -
                                                                                                                                                                                      outstation
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EMBL; X54102; CAA38036.1; -. EMBL; M94455; AAA32818.1; -. EMBL; AL161571; CAB81417.1;

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RESULT 5
RUNT_DROME
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Best Local
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P22814;
01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL035602; CAB38279.1;
PIR; S16527; S16527.
PIR; S16005; S16005.
PIR; S35240; S35240.
InterPro; IPR002068; Hsp20.
                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 Kania M.A., Bonner A.S., Duffy J.B., Gergen J.P.; "The Drosophila segmentation gene runt encodes a novel nuclear regulatory protein that is also expressed in the developing ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991
15-JUN-2002
                      FlyBase; FBgn0003300;
                                                                                                                                                                                                                                              -1- FUNCTION: PLAYS A PÍVOTAL ROLE IN REGULATING THE EXPRESSION OF OTHER PAIR-RULE GENES SUCH AS EVE, FTZ, AND H.
-1- SUBCELLULAR LOCATION: NUCLEAR:
-1- TISSUE SPECIFICITY: DEVELOPING CENTRAL AND PERIPHERAL NERVOUS
                                                                                                                                                                                                                                                                                                Nature 356:484-484(1992)
                                                                                                                                                                                                                                                                                                                         MEDLINE-92220161; Pu
Daga A., Tighe J.E.,
                                                                                                                                                                                                                                                                                                                                                  SIMILARITY TO AML1.
                                                                                                                                                                                                                                                                                                                                                                                      system."
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91065517; PubMed=2249771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Segmentation
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PROSITE; PS01031; HSP20; 1
                                 TRANSFAC;
                                                                                                                                                                                                                                                                                                            Leukaemia/Drosophila homology.";
                                                                                                                                                                                           DEVELOPMENTAL STAGE: MOST ABUNDANTI STAGE OF EMBRYOGENESIS.
SIMILARITY: CONTAINS 1 RUNT DOMAIN
                                                       A36392; A36392.
                                                                                                                                               European
                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shock; Chloroplast; Transit
SIT 1 19 CHLC
PF00853;
                                              060472;
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10; Conserv
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AASALCSPLAPSPSVS
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non-profit institutions as long
                                    T01066;
           IPR000040;
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Runt;
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41, Last
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          AML1_Runt.
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62.5%;
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Pred. No. 12;
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SMALL HEAT SHOCK PROTEIN
                                                                                                                                                                                                                       ABUNDANTLY EXPRESSED AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B25400AF6C01972E CRC64;
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Best Local S
Matches 8
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VARIANT
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                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nanba E., Suzuki K.;
"Organization of the mouse acid beta-galactosidase gene.";
Biochem. Biophys. Res. Commun. 178:158-164(1991).
-1- FUNCTION: CLEAVES BETA-LINKED TERMINAL GALACTOSYL RESIDUES FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galactosidase).
GLB1 OR GLB-1 OR BGL.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paragraphy (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Paragraphy (Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            GANGLIOSIDES, GLYCOPROTEINS, AND GLYCOSAMINOGLYCANS.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning of mouse acid beta-galactosidase cDNA: sequence, expression of catalytic activity and comparison with the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91298941; PubMed=1906271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bíochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nanba E., Suzuki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91076843; PubMed-2124109
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                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Lysosomal.
SIMILARITY: BELONGS TO FAMILY 35 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                            galactose residues in beta-D-galactosides
                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                               M57734;
M75122;
M75137;
M75107;
M75108;
M75109;
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| |||| ||:
|22 SPSILCSALPN 132
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8; Conser
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AAA37292.1;
AAA37292.1;
AAA37292.1;
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AAA37292.1;
AAA37292.1;
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AAA37292.1;
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200
359
31
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72.7%;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49676C6B63237C9F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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Best Local
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                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Hirst J., Bright N.A., Rous B., Robinson M.S.;

"Characterization of a fourth adaptor-related protein comp
"Characterization of a fourth adaptor-related protein comp
Mol. Biol. Cell 10:2787-2802(1999).

-i- FUNCTION: SUBUNIT OF NOVEL TYPE OF CLATHRIN-OR NON-CL/
ASSOCIATED PROTEIN COAT INVOLVED IN TARGETING PROTEIN:
                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
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CARBOHYD
CARBOHYD
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CARBOHYD
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ACT_SITE
ACT_SITE
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001944; GH_35.

Pfam; PF01301; Glyco_hydro_35; 1.

PRINTS; PR00742; GLYCOSYL_HYDROL_F35;

PROSITE; PS01182; GLYCOSYL_HYDROL_F35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BL; M75114; AAA37292.1; J
BL; M75115; AAA37292.1; J
BL; M75115; AAA37292.1; J
BL; M75117; AAA37292.1; J
BL; M75118; AAA37292.1; J
BL; M75119; AAA37292.1; J
BL; M75121; AAA37292.1; J
                              SIMILARITY).

SIMILARITY).

SUBUNIT: ADAPTER-LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER SUBUNIT: ADAPTER-LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER COMPOSED OF TWO LARGE CHAINS (EPSILON/AP4E1 AND BETA/AP4B1).

MEDIUM CHAIN (MU/AP4M1) AND A SMALL CHAIN (SIGMA/AP4S1).
                 SUBCELLULAR LOCATION: ASSOCIATED SIMILARITY).
SIMILARITY: BELONGS TO THE ADAPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:88151;
                                                                                                                                                                                                                                                                                                                                                       Ģ
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                                                                                                                                                                                                                                                                                                                                                                           Similarity 70.07; Conservative
                                                                                                                                                                                                                                                                                                                                     | CSPLPSLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosidase;
                                                                                                                                                                                                       (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĄ;
                                                                                                                                                                                    Chordata; Rodentia;
                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                   73121
                                                                                                                                                                                                                                                                                                                                                                                      52.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lysosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOINED
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                  THE ADAPTOR
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N-LINKED (GLCNAC. ..
N-LINKED (GLCNAC. ..
N-> D (IN REF. 2).
G-> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                     Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOPHILE (POTENTIAL)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA-GALACTOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                   0E68EAA66A10803A
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _F35; 1.
Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DONOR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 46;
                  COMPLEXES
                                                                                                                                                                                                                                    subunit
                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                  LARGE SUBUNITS
                                                                                   OR NON-CLATHRIN-
FROTEINS FROM T
SOSOMAL SYSTEM
                                                                                                                                                                                                                                    (Beta
                                                                                                                                                                                                                                                                                                                                                                            Indels
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(POTENTIAL).
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(POTENTIAL).
                                                                                                                                                                                     Euteleostomi;
; Murinae; Mus
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                                                                                                                           complex.";
                                                                                                                                                                                                                                    subunit
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RESULT
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Best Local S
Matches 10
             EMBL; 246843; CAA86882.1; -
EMBL; X92517; CAA63294.1; -
EMBL; Z71420; CAA96027.1; -
SGD; S0005088; YNL144C.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                            SEQUENCE FY1679;
STRAIN=588c / FY1679;
STRAIN=56287653; PubMed=8686380;
MEDLINE=56287653; PubMed=8686380;
Nasr F., Becam A.-M., Herbert C.J.;
"The sequence of 36.8 kb from the left arm of chromosome XIV reveals
"The sequence open reading frames: 18 correspond to new genes, one of
24 complete open reading frames: 18 correspond to new genes, one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNO4_YEAST
P53907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mallet L., Bussereau F., Jacquet M.;
Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts adenosine deaminase gene and 14 new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
101-OCT-1996 (Rel. 34, Last annotation update)
11990thetical 84.2 kDa protein in MFA2-MEP2 intergenic region
11990thetical 84.2 kDa protein in MFA2-MEP2 intergenic region
11990thetical 84.2 kDa protein in MFA2-MEP2 intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF155157; AAD43327.1; -. MGD; MGI:1337130; Ap4b1. InterPro: IPR002553; Adaptin_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
earcharomycetales: Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01602; Adaptin_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenosine deaminase gene and
Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96109932; PubMed=8619318,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                               Yeast 12:169-175(1996)
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                                                                                                                                                                                                                                                                          SIMILARITY: TO YEAST YHR131C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSILCSPL--PSLSLS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKQILCSPKSDPSLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocytosis.
39 AA; 82618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adaptin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1; Length 739; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1007D972BF8D0897 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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740 AA;

84202 MW;

7A3D75999DC83D06 CRC64;

Matches

Mismatches

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Gaps

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Best Local
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hiller L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Eukaryota, Metazoa, Ner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable 3',5'-cyclic phosphodiesterase R08D7.6
                                                                                                                                          InterPro; IPR003018; GAF.
InterPro; IPR003607; ME_Pplase_HDc.
InterPro; IPR002073; PDEase.
Pfam; PF00233; PDEase; 1.
Pfam; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                             PROSITE; PS00126; PDEASE_I; 1.
Hypothetical protein; Hydrolase;
SEQUENCE 918 AA; 104238 MW;
                                                                                            PRINTS; PR00387; PDIESTERASE1
SMART; SM00065; GAF; 1.
SMART; SM00471; HDC; 1.
                                                                                                                                                                                                                                        PIR; S24462; S24462.
PIR; S41041; S41041.
                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P30645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNE6_CAEEL
                                                                                                                                                                                                                            WormPep; R08D7.6;
                                                                                                                                                                                                                                                                          EMBL; 212017; CAA78052.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleoside 5'-phosphate.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FAMILY. STRONG, TO MAMMALIAN TYPE 6 CGMP PHOSPHODIESTERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSILCSPLPSLSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD
                                                                                                                                                                                                                            CE01047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%;
53.3%;
52.0%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
Score 39; DB Pred. No. 67;
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                                               CA59910AF4CD6155 CRC64;
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                                                                CGMP
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. No. 53;
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             Length 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 3.1.4.17).
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                                                                                                                                                                                                                                                                                                                       .isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shownkeen
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RESULT 10

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MU3C_ANASP STANDARD; PRT; 120 AA

Q44239; Q9WVX6;

01-NOV-1997 (Rel. 35, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howitt C.A., Whelan J., Price G.D., Day D.A.; "Cloning, analysis and inactivation of the ndhk gene encoding a subunit of NADH quinone oxidoreductase from Anabaena PCC 7120."; Eur. J. Biochem. 240:173-180(1996).
-!- CATALYTIC ACTIVITY: NADH + plastoquinone ~ NAD(+) + plastoquinol.-!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-A.sp. PCC 7120;
MEDLINE-21595285; PubMed-11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
7.707 TES=A.Sp. PCC 7120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and characterisation of the ndhCKJ-cluster of cyanobacteria Anabaena sp. PCC 7120."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                             Pfam; PF00507; oxidored_q4; 1.
Oxidoreductase; NAD; Plastoquinone; Complete
CONFLICT 87 87 H -> N (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES-A.variabilis; STRAIN-PCC 7937 / ATCC 29413;
Happe T., Schiefer W., Boehme H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADH-plastoquinone NDHC OR ALL3842.
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-A.sp. PCC 7120;
MEDLINE-96390878; PubMed-8797851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-A.sp. PCC 7120
Happe T., Schiefer W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120), and Anabaena variabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation and characterisation of the ndhCKJ gene-cluster variabilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. SPECIES-A.sp. PCC 7120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690, 1172;
                                                                                                                                                             EMBL; U31208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 84-120 FROM N.A. SPECIES=A.sp. PCC 7120;
                                                                                                                         interPro; IPR000440; Oxidored_q4.
                                                                                                                                                                                AJ012180; CAB45639.1; -. AP003594; BAB75541.1; -. AJ012181; CAB45646.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OCT-1998) to the EMBL/GenBank/DDBJ databases
120 AA;
                                                                                                                                                             AAC44352.1;
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oxidoreductase chain 3 (EC
   13621 MW;
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   574B662EAFF69BB2 CRC64;
                                    proteome.
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GRHR_SHEEP
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APC4_MOUSE
                                                                                                                                          RESULT 12
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Best Local
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                                                                                                                                                                                                                                       Best
                                                      P32237;
01-OCT-1993 (Rel. 27, Ca
01-OCT-1993 (Rel. 27, La
15-DEC-1998 (Rel. 37, La
Gonadotropin-releasing)
                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                               GNRHR
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APC4_MOUSE Q61268;
                                                                                                                   GRHR_SHEEP
                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                          Plasma; Lipid transport; Glycoprotein; Signal SIGNAL 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                               EMBL; Z24722; CAA80850.1; -. MGD; MGI:87878; Apoc4.
                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94375002;
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STRAIN=C57BL/6; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apolipoprotein
                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                          Local Similarity hes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: LIVER.
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Caprinae;
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107
124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         el. 40, Last annotation update)
C-IV precursor (Apo-CIV) (Apolipoprotein C2-linked)
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                    27, Created)
27, Last sequence update)
37, Last annotation update)
asing hormone receptor (GNRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8088778;
                                                                                                                                                                                                                                                                     124
107
14288
 Ovis.
                        Chordata; Craniata; Vertebrata; Euteleostomi;
             Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.7%;
58.3%;
                                                                                                                                                                                                                                     50.7%;
58.8%;
                                                                                                                                                                                                                                                                        MW;
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                                                                                                                                                                                                                                     Score 38;
Pred. No.
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Pred. No.
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97C3CDEE72C9A452 CRC64;
                                                                                                                                                                                                                                                                                              APOLIPOPROTEIN C-IV.
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                                                                                                                   328
             Ruminantia;
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              Pecora;
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; Murinae; Mus
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EMBL; L22215; AAC37336.1; -.
EMBL; X72088; CAA50978.1; -.
EMBL; X42937; AAB38515.1; -.
EMBL; L43842; AAB41939.1; -.
EMBL; L43842; AAB41939.1; JOINED.
EMBL; L43841; AAB41939.1; JOINED.
PIR; JN0882; JN0882
InterPro; IPR000276; GPCR_Rhodpsn.
  CARBOHYD
CARBOHYD
DISULFID
                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Pituitary;

MEDLIND-94059099; PubMed-7694577;

Illing N., Jacobs G.F.M., Becker I.I., Flanagan C.A., Davidson in the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-Scottish blackface; TISSUE-Pituitary;
MEDLINE-94040345; PubMed-8224516;
Brooks J., Taylor P.L., Sauders P.T.K., Eidn
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campion C.E., Turzillo A.M., Clay C.M.;
"The gene encoding the ovine gonadotropin-releasing receptor: cloning and initial characterization.";
Gene 170:277-280(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hormone receptor and clestrous cycle.";
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                                                                               TRANSMEM
                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequencing of the Simple re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO FAMILY 1 OF G-PRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MESSENGER SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNCTION: THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
                                                                                                                                                                                                                                                                                                                                                                           PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biophys. Res. Commun. 196:745-751(1993).
                                                                                                                                                                                                                                                                                                                                                               coupled
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receptor;
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                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
                                                                                 EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                                                                                            EXTRACELLULAR (POTENTIAL) 5 (POTENTIAL).
                                                                                                                                                                                                    4 (POTENTIAL)
                                                                                                                                                                                                                       CYTOPLASMIC
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3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                        ransmembrane; Glycoprotein.
EXTRACELLULAR (POTENTIAL).
                                                                               (POTENTIAL)
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RESULT 13
IRLS_BURPS
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Best Local Similarity
Watches 10; Conserv
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                                                                                     Pfam; PF00512; signal; 1.
Pfam; PF00572; HAMP; 1.
Pfam; PF00578; HATPase_C; 1.
Pfam; PF00344; BCTRLSENSOR.
SMART; SM00304; HAMP; 1.
SMART; SM00388; HATPase_C; 1.
SMART; SM00388; HiskA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                               "Identification and characterization of a two-component regulatory system involved in invasion of eukaryotic cells and heavy-metal resistance in Burkholderia pseudomallei.";

Infect. Immun. 65:4972-4977(1997).

-i- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM IRLR/II

-i- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM IRLR/II

RESISTANCE. PROBABLY ACTIVATES IRLR BY PHOSPHORYLATION.

-i- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Sensor protein irlS (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRLS_BURPS 031396;
                                 TRANSMEM
                                                       Transmembrane;
                                                                 PROSITE; PS50109; HIS_KIN; 1. Sensory transduction; Transferase; Kinase;
                                                                                                                                                                                                                             EMBL; AF005358; AAB92483.1;
                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-1026b;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia
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                                             DOMAIN
                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                      DOMAIN
                                                                                                                                                                                             InterPro;
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                                                                                                                                                                   o; IPR003594; ATPbind_ATPase.
o; IPR004358; Bact_sens_pr_C.
o; IPR003660; HAMP.
o; IPR003661; His_KIN_sig.
o; IPR003661; His_kinA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Pseudomonas pseudomallei).
beta subdivision; Burkholderia
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         CYTOPLASMIC POTENTIAL.
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Pred. No.
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S -> R (IN REF. 2).
T -> A (IN REF. 2).
A -> G (IN REF. 2).
0618374F33ECC6FE CRC64;
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                      (POTENTIAL)
                                          (POTENTIAL)
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ROOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RS
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RS
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hunt S., Jagels K.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hunt S., McLean J.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hunt S., McLean J.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hunt S., McLean J.,
RA
Gentles S., Goble A., Hamlin N., Harris D., Hunt S., McLean J.,
RA
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA
Moliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA
Multerford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA
RA
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA
RA
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA
Raklton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA
RA
Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA
RA
Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA
Moodward J., Volckaert G., Holzer E., Moestl D., Hilbert H.,
RA
Moodward J., Volckaert G., Holzer E., Moestl D., Hilbert H.,
RA
Moodward J., Vanner J., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA
Gerry P., Zimmerman W., Wedler H., Wambutt R., Purnelle B.,
RA
Gerry C., Schole E., Dreano S., Glows S., Lehrach H., Reinhardt R.,
RA
Lucas M., Rochet M., Galllardin C., Tallada V.A., Garzon A., Thode G.,
RA
Cerry M., Moestles J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA
Cerry M., Charles J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA
Cerry M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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SEQUENCE
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                     This SWISS-PROT entry is copyright. It is produced through a collar between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                      Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Pot Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                    DNA Res. 4:363-369(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
                                                                                                                                                                                                                                                         MEDLINE=98162722; PubMed=9501991; Yoshioka S., Kato K., Nakai K., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 198-554 FROM
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Pred. No.
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PHOSPHORYLATION (AUTO-) (
C4FE275489AEDCBD CRC64;
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       not
                                                                                                                                                                                                                                 Okayama H., Nojima H.; frames in Schizosaccharomyces
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MBL outstation -
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TRPX_ARATH
ID TRPX_A
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DE ARCHARY
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STRAINECY. Columbia;
STRAINECY. Columbia;
STRAINECY. Columbia;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.U.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Goodman H.M., Scitco C. Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p32069;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                              "Two anthranilate synthase genes in Arabidopsis: defense-related regulation of the tryptophan pathway."; plant Cell 4:721-733(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddioctyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anthranilate synthase component (EC 4.1.3.27).
ASA2 OR AT2G29690 OR T27A16.21.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93005721; PubMed=1392592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                      Niyogi K.K., Fink G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
  THE 402:761-768(1999) CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D89115; BAA13777.1; -.
Pro; IPR002293; AA/rel_prmease1.
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7; Conserv
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                                                        and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR004840; AAc_permease. IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
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Chorismate
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A -> D (IN REF. 2).

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A -> G (IN REF. 2).

P -> A (IN REF. 2).

A -> D (IN REF. 2).
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Search completed: June 25, 2003, 17:15:58 Job time: 2.6443 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005256; Anth_synthI.
InterPro; IPR000350; Chorismate_bind.
Pfam; PF00425; Chorismate_bind; 1.
PRINTS; PR00095; ANTSNTHASEI.
ProDom; PD000779; Chorismate_bind; 1.
TIGRFAMS; TIGR00564; trpE_most; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tryptophan biosynthesis; Lyase; Chloroplast; Transit peptide; multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S27752; S27752.
HSSP; Q06128; 1QDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M92354; AAA32739.1; -. EMBL; AC005496; AAC35228.1; -.
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PATHWAY: Tryptophan biosynthesis; first step.

SUBGUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II.

SUBCELLULAR LOCATION: Chloroplast (Probable).

MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAMILY.
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69815 MW;
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69.2%;
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ANTHRANILATE SYNTHASE COMPONENT I-2
                                                                                                                                                                                                                                                                                                                                                                                                                              D4039FE58A420967 CRC64;
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sp_rvirus:*
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                              Q15134 homo sapien
Q8w6el bacteriopha
Q9n7d6 leishmania
Q96eh4 homo sapien
                                                                   Q9suy8 arabidopsis
08r4h6 mus musculu
Q9jms9 escherichia
08x3q9 escherichia
09maa0 arabidopsis
Q8w0z7 arabidopsis
Q8w0z7 arabidopsis
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| \vdash | Q9p960 aspergillus | | Q9f804 erwinia amy | 5 marm | Q8wy82 homo sapien | homo | Q9p0f9 homo sapien | . Q8qhnl peaton viru | peaton | | | Q8qz58 kaikalur vi | Q9lpk3 arabidopsis | O94837 homo sapien | 9 | ຜ | | Q8tfe4 gaeumannomy | | O80871 arabidopsis | Q9n223 gorilla gor | Q8s7g3 oryza sativ | Q9ad17 polyangium | Q9usn1 schizosacch | mus | mus muscul | O83294 treponema p | Q9ph15 xylella fas |

ALIGNMENTS

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RESULT 2
Q8R4H6
ID Q8R4
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Q9SUY8;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 53.0 kDa protein.
F4F15.280
    Q8R4H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 490 AA; 5
                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL049711; CAB41337.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                   1 SSSILCSPLPSLSLS 15
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11; Conservative
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    PRELIMINARY;
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73.3%;
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01-JUN-2002
01-JUN-2002
01-JUN-2002
MEDLINE-9537425; PubMed-7612932;

Broom J.E., Hill D.F., Hughes G., Jones W.A., Stockwell P.A., Petersen G.B.;

"Sequence of a transposon identified as Tn1000
                                                                                                                                                                                                                                                                                        Yoshioka Y., Fujita Y., Ohtsubo E.;
"Nucleotide sequence of the promoter-distal region
of plasmid R100, including trai (DNA helicase I) an
J. Mol. Biol. 214:39-53(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimizu H., Saitoh Y., Suda Y., Uehara K., Sampei G. "Complete nuclectide sequence of the F mlasmid: Its organization and diversification of plasmid genomes. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Himmel K.L., Bi F., Shen H., Jenkins N
Largaespada D.A.;
"Activation of Clg, a Novel Dbl Family
"Activation at Factor Gene, by Proviral Insertion at
                                                                                                                                                                 MEDLINE-87194554; PubMed-3032897;
Saadi S., Maas W.K., Hill D.F., Bergquist P.L.;
"Nucleotide sequence analysis of RepFIC, a basi
IncFI plasmids P307 and F, and its relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel.
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-90317835;
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Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Shimizu H., Saitoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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Cell Chem. 277:13465-13472(2002).

AF465238; AAL93134.1; -

NCE 1298 AA; 139193 MW; 3451)
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                                                                                                                         169:1836-1846(1987).
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Q8X3Q9;
01-MAR-2002
01-MAR-2002
                             SEQUENCE
                                                                                                STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eichenlaub
"F Plasmid
                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=0157:H7 / E
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiol. Rev. 58:162-210(1994). EMBL; AP001918; BAA97892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manwaring N.P., Skurray R.A., "Nucleotide sequence of the F Plasmid 41:219-225(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       partition of plasmid mini-F.";
J. Bacteriol. 165:1043-1045(1986).
                                                                                                                                                                                                                     Bacteria;
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                                                  Pfam;
                                                                      EMBL;
                                                                              Nature 409:529-533(2001)
                                                                                                                                                                                                             Escherichia
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                                                                      Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8W0Z7;
                                                                                                                                                                                                                                                                                                                             (AT3905190/T12H1_16).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative branched-chain amino acid aminotransferase.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSLLSSPLPPPSLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSIICSPMTSLKTSI
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                                                    (DEC-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54829 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.3%;
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                                             the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D29B6878564B36BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555
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                                                                                                                                                                                                                                                                                                                                                              eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                  Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                              Rosidae;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                              InterPro; IPR001882; Biotin_attach.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000089; Biotin_Carb_C;
Pfam; PF02785; Biotin_carb_C; 1.
Pfam; PF00288; CPSase_L_chain; 1.
Pfam; PF02786; CPSase_L_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91ZA3; PRELIMINARY; PRT; /24 AA.
Q91ZA3;
Q1-DEC-2001 (TrEMBLrel 19, Created)
Q1-DEC-2001 (TrEMBLrel 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL; AF462849; AAL58936.1; EMBL; AY090279; AAL90940.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Led J.M., Jin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                PROSITE; PS00188; BIOTIN; UNKNOWN_1.
PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
SEQUENCE 724 AA: 79660 MM; DB5EC4C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and its rescue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF01063; aminotran_4; 1.
ProDom; PD001961; Aminotran_4; 1.
Aminotransferase, Transferase.
SEQUENCE 555 AA; 62212 MW; 67/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 0:0-0(2001).
EMBL; AY046947; AAL02364.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionyl CoA-carboxylase alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY090279; AAL90940.1; -. InterPro; IPR001544; Aminotran_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Fatal propionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miyazaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Arabidopsis ORF clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim C.J., Chen H., Cheuk R., Meyers M.C.,
  654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
11; Conserv
                                                                                                 Similarity
8; Conserv
TSSTLCSPMPGVVVAV
                                                 SSSILCSPLPSLSLSV 16
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by postnatal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acidemia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                         61.3%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
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  669
                                                                                                                                                                                             UNKNOWN_1.
W; DB5EC4CBF40739FB CRC64;
                                                                                                 5
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                                                                                                                         Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mice lacking propionyl-CoA Carboxylase liver-specific supplementation via a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670A17B8D74B5D86 CRC64;
                                                                                                 Mismatches
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                                                                                                                         No. 11;
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8.7;
                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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Goldsmith A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
                                                                                                                                              Length 724;
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                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Satou
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G
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RESULT Q922N3 ID Q9 AC Q9

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Q922N3; Q922N3;

PRELIMINARY;

PRT;

724

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A Strausberg R.;

(L Submitted (APR-2001) to the EMBL/GenBank/DDB5 usumitted (APR-2001) to the EmbL/GenBank/DDB5 u
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                        ALD DAR REPORTED TO THE PROPERTY OF THE PROPER
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Best Local S
Matches 8
Pfam; PF00613; PI3Ka; 1.

Pfam; PF00792; PI3K_C2; 1.

Pfam; PF00454; PI3_PI4_kinase; 1.

SMART; SM00239; C2; 1.

SMART; SM00145; PI3Ka; 1.

SMART; SM00146; PI3Kc; 1.

SMART; SM00142; PI3K_C2; 1.

SMART; SM00142; PI3K_C2; 1.

PROSITE; PS00915; PI3_4_KINASE_1; 1

PROSITE; PS00916; PI3_4_KINASE_3; 1

PROSITE; PS00916; PI3_4_KINASE_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q15134
Q15134;
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01-DEC-2001 (TrEMBLrel. 19, La
01-JUN-2002 (TrEMBLrel. 21, La
Similar to propionyl coenzyme
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Volinia S.;
Submitted (DEC-1994) to the
EMBL; Z46973; CAA87094.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-280 FROM N.A.

MEDLINE-95354652; PubMed-7628435;

Volinia S., Dhand R., Vanhaesebroeck B., MacDougall L.K.,

Zvelebil M.J., Domin J., Panaretou C., Waterfield M.D.;

"A human phosphattidylinositol 3-kinase complex related to Vps34p-Vps15p protein sorting system.";

EMBO J. 14:3339-3348(1995).
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01-NOV-1996 (TrEMBLTel. 01, La
01-DEC-2001 (TrEMBLTel. 19, La
Phosphatidylinositol 3-kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000008; C2.
InterPro; IPR001263; PI3Ka.
InterPro; IPR002420; PI3K_C2.
InterPro; IPR000403; PI3_PI4_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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8; Conserv
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19, Last sequence update)
21, Last annotation update)
enzyme A carboxylase, alpha
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RESULT 10
Q8W6E1
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Q9N7D6
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Best Local Similarity
"-+ ches 10; Conserv
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Best Local S
Matches 6
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Q8W6E1;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
                                                                                                                                                                                                                              Murphy L., Quail M., Harris D., R. Submitted (JUL-2000) to the EMBL/EMBL, AL39035; CACO1001.1; -InterPro; IPR000719; Euk_pkinase. ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9N7D6 PRELIMINARY; PRT; 138 AA.
Q9N7D6;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Possible serine/threonine kinase pkn8 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sinha K.K., Ghosh A.; "Complete nucleotide sequence of single-stranded filamentous vibriophage VSK"; submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF452449; AAL40839.1; -
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Viruses; ssDNA viruses; Inoviridae
NCBI_TaxID=180503;
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Eukaryota; Euglenozoa;
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                                                                                                                                                                                                                     Kinase.
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ENCE 82
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6; Conser
SSSILCSPLPSLSLS
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138 AA;
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66.7%;
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54.5%;
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69.2%;
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20,
                                                                                                                                                                                                                                                                                                 D., Rajandream M.,
EMBL/GenBank/DDBJ
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Last annotation update)
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Pred. No.
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                                                                                     Pred. No.
                                                                                                       Score 43;
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Pred. No.
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                                                                                                                                                 2AF74AF4488B12D6 CRC64;
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4.7;
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                                                                                                       Length 138;
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Matches
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                                                                InterPro: IPRO00152; Asx.hydroxyl.
InterPro: IPRO00156; EGF-like.
InterPro: IPRO00742; EGF_2.
InterPro: IPRO01881; EGF_Ca.
InterPro: IPRO01438; EGF_II.
InterPro: IPRO01438; EGF_II.
InterPro: IPRO01759; Pentaxin.
InterPro: IPRO00436; Sushi_SCR_CCP.
InterPro: IPRO000436; Sushi_SCR_CCP.
InterPro: IPRO000436; Sushi_SCR_CCP.
InterPro: IPRO000436; Sushi_SCR_CCP.
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Q96ЕН4;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                        Biochem. J. 352:49-59(2000).
EMBL: AF206329; AAG32160.1;
HSSP; P00740; 1EDM.
MGD: MGI:1928849; Polydom.
                                                                                                                                                                                                                                                               MEDLINE-20517255; PubMed-11062057; Gilges D., Vinit M.-A., Callebaut I.,
                                                                                                                                                                                                                                                                               STRAIN-C3H/HENSIC; MEDLINE-20517255;
                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                          Polydom protein precursor. POLYDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ES77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC012330; AAH12330.1; -. SEQUENCE 189 AA; 19503 MW; BC1D0F5B688D62E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
Similar to RIKEN cDNA 4933430F08 gene.
                                Pfam;
Pfam;
                                                                                                                                                                                                                                  protein,
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                         Pfam;
                                                                                                                                                                                                                                             "Polydom :
                                                                                                                                                                                                                                                         Romeo P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                              PF00008; EGF; 10.
PF02494; HYR; 2.
PF00354; pentaxin; 1.
         PF00084; sushi; 33. PF00092; vwa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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EGFBLOOD
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71.4%;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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nd von willebrand
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Matches 9
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PRINTS; PRO0453; VWFADOMAIN.
PRODOM; PD002153; Pentaxin; 1.
SWART; SM00032; CCP; 34.
SMART; SM00181; EGF; 15.
SWART; SM00179; EGF; CA; 9.
SWART; SM00179; EGF_CA; 9.
SWART; SM00001; EGF_Like; 3.
SWART; SM00327; VWA; 1.
                 Q9YBN2
Q9YBN2;
Q1-NOV-1999
01-NOV-1999
01-MAR-2002
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O9OWV3
OPTELIMINARY; PRT; 113 AA.
O9OWV3
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS00022; EGF_1; UNKNOWN_9.
PROSITE; PS01186; EGF_2; 11.
PROSITE; PS01187; EGF_CA; 6.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                       EMBL;
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ROWEN L., Qin S., Madan A., Loretz C., James R., Dors M., Mi Hall J., Lasky S., Hood L.;

"Sequence of the mouse major histocomaptibility locus class
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090; '
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DAXX OR DAXX.
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                                                                                                                                                                                                                                  itted (OCT-1998) to the ; AF100956; AAC69891.1; MGI:1197015; Daxx. rPro; IPR005012; Daxx.
                                                                                                                                                                                                                         PF03344; Daxx;
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3567 AA;
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9 (TrEMBLrel. 12,
2 (TrEMBLrel. 20,
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69.2%;
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62.5%;
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                   Last annotation update)
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                                         Created)
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                            Last sequence
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Pred. No.
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W; 8FBA8276E12293E5 CRC64;
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Hypothetical APE1566.

protein APE1566.

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OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;

OC Desulfurococcaceae; Aeropyrum.

OX NCBL_TaxID=56636;

RN [1]
RP SEDGE FROM N.A.

RP SEDGE FROM N.A.

RC STRAIN-K1;

RA KAWATABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,

RA KAWATABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,

RA HOSOYAMA A., FUKUI S., NAGAI Y., NIShIJAMA K., NAKAZAWA H.,

RA HOSOYAMA A., FUKUI S., NAGAI Y., NIShIJAMA K., NAKAZAWA H.,

RA YAMAZAKI J., KUSHIGA N., OGUCHI A., AOKI K.-I., KUDOTA K.,

RA YAMAZAKI J., KUSHIGA N., OGUCHI A., AOKI K.-I., KUDOTA K.,

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RA YAMAZAKI J., KUSHIGA N., OGUCHI A., AOKI K.-I.,

RA YAMAZAKI J., KUSHIGA N., OGUCHI A., AOKI K.-I.,

RA YAMAZAKI J., KUSHIGA N.,
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Result
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is derived by analysis of the total score distribution.
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US-08-417-30A-17

US-09-002-361-7

US-09-002-361-7

US-08-137-614A-3

US-08-417-30A-13

US-08-417-30A-13

US-08-417-30A-11

US-08-417-30A-11

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US-08-072-064-2

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US-08-072-064-5
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PCT-US96-06035-5
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| 97.8 | 97.8 | 101.6 | 101.6 | 102.8 | 106.2 | 106.2 | 106.2 | 106.2 | 106.2 | 106.2 | 109 | 111.2 | 111.2 | 119.6 | 119.6 | 119.6 | 124 |
| 6.0 | 6.0 | 6.2 | 6.2 | 6.3 | 6.5 | 6.5 | 6.5 | 6.5 | 6.5 | 6. 5 | 6.6 | 6.8 | 6.8 | 7.3 | 7.3 | 7.3 | 7.6 |
| 1479 | 1479 | 1917 | 1917 | 762 | 2601 | 2601 | 2544 | 2544 | 2508 | 2508 | 2635 | 1542 | 1542 | 2059 | 1970 | 1970 | 1707 |
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| PCT-US95-06556-2 | US-08-249-112-2 | US-09-436-063C-6 | US-09-627-650B-6 | US-09-592-891A-7 | US-09-436-063C-10 | US-09-627-650B-10 | US-09-436-063C-4 | US-09-627-650B-4 | US-09-436-063C-8 | US-09-627-650B-8 | US-08-768-301-3 | PCT-US95-06556-1 | US-08-249-112-1 | PCT-US92-08558-2 | PCT-US92-08558-3 | US-08-072-064-9 | US-08-809-802-7 |
| Sequence 2, Appli | Sequence 2, Appli | Sequence 6, Appli | Sequence 6, Appli | Sequence 7, Appli | Sequence 10, Appl | Sequence 10, Appl | Sequence 4, Appli | Sequence 4, Appli | 80 | Sequence 8, Appli | Sequence 3, Appli | Sequence 1, Appli | Sequence 1, Appli | Sequence 2, Appli | Sequence 3, Appli | Sequence 9, Appli | Sequence 7, Appli |

ALIGNMENTS

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; NAME/KEY: Coding Sequence LOCATION: 47...1402 ; OTHER INFORMATION: US-08-809-802-11
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US-08-809-802-11
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                                                                                                                                                                                                                                                                                                                                                   ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809/802
FILING DATE: 19-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02323
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Yablonsky, Michael D
REGISTRATION NUMBER: 40,407
REFERENCE/DOCKET NUMBER: T1292
                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1555 base pairs
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                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4678
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Le Bourdelles, Beatrice
APPLICANT: Whiting, Paul John
TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT
TITLE OF INVENTION: OF THE GABA-A RECEPTOR
NUMBER OF SEQUENCES: 14
                                                                                      MOLECULE TYPE: CDNA FEATURE:
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COUNTRY: USA
ZIP: 07065-0900
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                                                                                                                                                     STRANDEDNESS:
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Pred. No. 6.3e-47;
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APPLICANT: Xavier Georges Sarda
APPLICANT: Whichel David Tomalski
APPLICANT: Whichel David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Rece
FILE REFERENCE: A32815 072667.0118
FULC REPRIATE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 14
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13 CCAGCGGTAGTGAGCGTCAATATTTGTCCGAAGTATATCAAAGATCGATGACGTCACA CCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACA CGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAG ATGGAATACTCCGTACAGTTAACGTTTCGGGAACAATGGTTAGATGAACGGCTCAAATTC AAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATT CCTGATCTATTCTTCTCCAACGAGAAGGAAGGTCATTTCCACAACATCATCATGCCGAAC CCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCCAACTTCCATGAGGTGACCACGGACAAC ATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTAC CTTGAGAGCTCATCCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTAC TTGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAG GTGTACATCCGGATCTTCCCCCAACGGCAACGTGCTGTACAGCATCCGAATCTCCTTGACG AATAATCTTGGAGGTCGCCTCAAATACCTGACACTGACCGAAGCCAACAGAGTCTGGATG AGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATCGTGTCCTGGGTG CACTACAACACAGGGAAATTCACCTGCATGGAGGTAAAGTTTCACCTGGAACGGCAGATG GGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCCAAG ACCACAGACGACTTAGTGTTCCTATGGAAGGCGACC---CGGTGCAGGTGGTGAAN ACCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAG TCCTTCTGGCTGGACCAGGGAGCTGTGCCTGCGAGGGTCTCACTAGGAGTGACGACTTTA TCCTTCTGGATCAACATGGATGCTGCCCCTGCCCCTGTGGGCCTGGGGCATCACCACCGTG GGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTC AAGACTAATACCGGTGAATACAGTTGCCTGAAGGTAGACTTGCTCTTCAAACGCGAGTTC AACTTACACCTGCCTCGGTTCAC - - - GCTGGAGAAGTTCCTCACTGACTACTGCAACAGT Score 187; DB 4; Pred. No. 6.9e-45; 0; Mismatches 346 or Receptor 346; Length ----ATGGTTGG 48; Gaps 627 507 569 447 509 387 449 327 707 689 567 629 1001 821 747 764 687 927 867 881 807 941

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RESULT 3
US-08-417-330A-15
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GENERAL INFORMATION:
                                                                                        Query Match
Best Local Similarity
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                                                                            Matches 488;
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ADDRESSEE: J. MARK HAND - MERCK &
STREET: 126 EAST LINCOLN AVENUE -
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: TI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: NJ
COUNTRY: US
ZIP: 07065-0900
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                                                                                                                                                                 OTHER INFORMATION
                                                                                                                                                                               NAME/KEY: Coding Sequence LOCATION: 298...1683
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                                                                                                       Sequence 11, Application US/09592891A Patent No. 6329174 GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
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LENGTH: 1609
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SOFTWARE: FastSEQ for
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ORGANISM: Artificial Sequence
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Pred. No. 1.5e-43;
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US-08-435-933-5
; Sequence 5, Application
; Sequence 10, 5693492
; Patent NO. 5693492
; GENERAL INFORMATION:
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; TOPOLOGY: linear
; MOLECULE TYPE: CDN:
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TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3958 base pairs
TYPE: nucleic acid
GREANGENESS: 6:010
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Matches
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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NAME: Wallen, III John W.
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TITLE OF INVENTION: DNA ENCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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SOFTWARE: PatentI
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Arena, Joseph P.
Paress, Philip S.
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Pred. No. 1.4e-42;
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application PC/TUS9606035
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
FILING DATE:
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Glesser, Jody M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 1926
TELECOMMUNICATION INFORMATION:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Jody M. Giesser
STREET: 126 East Lincoln Avenue -
                                                                                                                                                                                                                                                                                            STREET: 126 E
CITY: Rahway
STATE: New Je
                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07065-0907
                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                              New Jersey
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Local Similarity 53.7%;
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                 GCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCG 1073
                                                   CCCGTTTCCTATACGAAGGCCATCGATGTGTGGACAGGCGTGTGTCTGACGTTCGTGTTC
                                                                                                                                                                                               ATTGTATCATGGGTATCATTCTGGCTGGATCAAGGAGCAGTACCGGCGCGAGTGTCACTG
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Conservative
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Pred. No. 1.4e-42;
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APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT APPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 1640
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-592-891A-12
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APPLICANT:
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GATGTACATCCCCAGCCTACTCATCCTGATCCTGGGTCTCCTTCTGGATCAACAT
                                                                       ATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCA
                                                                                                                                                                                                                                                                                                                                                                  CCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                    CCCCAACGCCAACGTGCTGCACACCATCCGAATCTCCCTGACGCTCTCGTGCCCCATGAA
                                                                                                                        GT---TCACGCTGGAGAAGTTCCTCACTGACTACTGCAACAGTAAGACTAATACCGGTGA
                                                                                                                                                          GTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAA
                                                                                                                                                                                            GTTCCTATGGAAGGAAGGCGACC---CGGTGCAGGTGGTGAAAAACTTACACCTGCCTCG
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                                                                                                                                                                                                                                                                                                                               CCTCAAGTTGTACCCCCTGGATAAGCAGACCTGCTCCTCAGGATGGCTAGTT-----
                                                    ATACAGTTGCCTGAAGGTAGACCTGCTCTTCAAACGCGAGTTCAGTTACTACCTGATCCA
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; Pred. No. 2.3e:
0; Mismatches
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2.3e-41;
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US-09-130-339-1
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Best Local Similarity
Matches 453; Conserv
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APPLICANT: Paress, Philip S.
APPLICANT: Warmke, Jeffrey W.
APPLICANT: Etter, Adrian
APPLICANT: Cohen, Charles J.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, PAICHARD ENCODING CTENOCEPHALIDES
TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS
FILE REFERENCE: 20029
FILE REFERENCE: 20029
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 8
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                     585 ACTOTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGT
                                                           519 TCTGAAACTGTATCCGCTCGATAGGCAGGTGTGCTCTCTCCGGATGGCCAGTTA-----
                                                                                                                               459 TCCTTACGGTTCCGTACTATACAGCATCAGGATATCGCTTACTTTGGCGTGTCCTATGAA
                                                                                                                                                 405 TAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTT
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                                                                                           CCTCAAGAACTTCCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCAT
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Pred. No. 1.4e-39;
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| AATGGACTACCGGGTGAATO CTGGAATACAGTGTCCAGG CCGAGAATATCCTGATGACG TAACGACTTTGGAGGTCGTO GCCAGACCTCTTTGGAGGTCGTO GCCAGACCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS FILE REFERENCE: 20029 CURRENT APPLICATION NUMBER: U\$/09/130,339 CURRENT FILING DATE: 1998-08-06 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 1297 TYPE: DNA ORGANISM: ctenocephalides felis S-09-130-339-3 Query Match Best Local Similarity 53.9%; Pred, No. 1.4e-37; Best Local Similarity 53.9%; Pred, No. 1.4e-37; | APPLICANT: Cully, Doris F. APPLICANT: Paress, Philip S. APPLICANT: Warmke, Jeffrey W. APPLICANT: Warmke, Jeffrey W. APPLICANT: Etter, Adrian APPLICANT: Cohen, Charles J. APPLICANT: Brochu, Richard M. TITLE OF INVENTINE. DAN MOLECULES ENCODING CTENOCEPHALINES | EESULT 9 18-09-130-339-3 18-09-130-339-3 Sequence 3, Application Patent No. 6358701 | Db 951 GACCGGAGTCTGCCTCACGTTCGTCTTCGGGGCTTTGCTCGAATTCGCCCTCGTCAACTA 1010 Qy 1065 TGTTTC 1070 Db 1011 GGCTTC 1016 | 945 GAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTG | Qy 825 GATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCTCCTTCTGGATCAACAT 884 | Qy 705 GTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAA 764 | Db 573 |
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| STATE: New York COUNTRY: USA ZIP: 11530-0299 COMPUTER READABLE FORM: MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-POS OPERATING SYSTEM: PC-DOS/MS-POS CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/554,659 FILING DATE: CLASSIFICATION: 436 | RESULT 10 US-08-554-659-3 Sequence 3, Application US/08554659 Patent No. 5767261 Patent No. 5767261 APPLICANT: Wingate, Vincent APPLICANT: Wolff, Mark PITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL TITLE OF INVENTION: AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: SCOILly, Scott, Murphy & Presser CITY: Garden City Plaza | Db 862 AAAAGCCATCGACGTCTGGACGCGAGTCTGCCTCACGTTCGTCTTCGGGGCTTTGCTCGA 921 Oy 1047 GTATGCTGCCATAAAATTTTGTTTC 1070 | QY 927 GCTCACCATGACCACCAGAGCTCTGGCTCCCGGCCTCTTTGCCTAAGGTGTCCTACGT 986 | 682 CTCGTACTACCTGATCCAGATCTACATTCCTTGCTTGCATGTTGGTGATCGTTTCCTGGGT 867 CTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGT | 747 GCACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGAT | Qy 627 CACCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCCAAGTGGCTGA 686 | Qy 507 TTTGTCCTGCCTGATGACCTCCAAGAACTTCCCCATGGACGTGCACGATGCA 566 | Db 310 GCCCGATTTGTTCTTTGCGAATGAAAAGGAGGCCACTTTCACAACATCATCATGCCGAA 369 Qy 447 CAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCAT 506 |

ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S

DiGiglio, Frank

REGISTRATION NUMBER:

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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity
Matches 474; Conserv
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TCCTGTCCTGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCCTGG
                                                                    TGGAACGGCAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCA
                                                                                                      CCATGGAGATTTCTC---TTACGACAGGAAACTACTCTCGTCTGGCATGTGAAATTCAAT
                                                                                                                                       GCTGTTGTACCAAGCACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTCACC
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                                  TTGTAGGCTCGATGGGATACTATTTAATTCAGATTTATATTCCGTCTGGCCTAATTGTCA
                                                                                                                                                                         TGGGTGTGTCGAGCGAAGTGTCTTTGCCGCAATTCAAGGTGCTGGGCCACCGGCAGCGGG
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(516) 742-4366
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                                                                                                           Query Match
Best Local Similarity
                                                                                              Matches 474;
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dechert Price & Rhoads STREET: 997 Lenox Drive, Building CITY: Lawrenceville
                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                             OTHER INFORMATION
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        ENGTH:
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                               ATATCTCAGCCATTTTGGATTCGCTAAGTGTAAGCTACGACAAAAGAGTGAGGCCGAACT
                                                            ATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATT
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                                                                                                                                                                                             Coding Sequence 104...1591
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                                                                                          Score 157.8; DB 4;
Pred. No. 1.7e-36;
0; Mismatches 397;
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RESULT 12
US-08-417-330A-19
                                                                                                                                                                    Sequence 19, Application US/08417330A Patent No. 5719057
                                                                                                                                                    GENERAL INFORMATION:
                                                                   APPLICANT: HADINGHAM, KAREN
APPLICANT: LE BOURDELLES, BEATRICE
APPLICANT: WHITING, PAUL
APPLICANT: WINGROVE, PETER
                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                              974
                                                                                                                                                                                                                                                                                                                                                                                                                                   963
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   SEQUENCES:
STABLY TRANSFECTED CELL LINE EXPRESSING GABA-A RECEPTOR AND NOVEL CLONED GABA-RECEPTOR SUBUNIT CDNA SEQUENCES 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 460;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:

NAME: HAND, MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: T11(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10F0RMATION:
TELECOMMUNICATION 10F0RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US
FILING DATE: 05 APR-1S
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 126 E
CITY: RAHWAY
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding LOCATION: 225...1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: J. MARK HAND - MERCK & STREET: 126 EAST LINCOLN AVENUE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                            GAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAG
                                                                                                                                                                                                                                                                                  CTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAAT
 TGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTT
                                                                                                                                                                                     GATAAGAAGTCATTTGTGCACGGAGTGACTGTTAAGAACCGCATGATTCGCCTGCATCCT
                                                                                                                                                                                                                                                                                                                                                                       TTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCT 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCTATGACATTCGTCTGAGACCAGATTTTGGAGGTCCCCCCGTGGCTGTGGGGATGAAC
                                    AGGAGGTACCCACTGGATGAACAAAACTGCACCTTGGAAATTGAGAGCTA-------
                                                                                                                                                                                                                                                             -TGACTCTGGACAACAGAGTGGCAGACCAGCTCTGGGTGCCTGATACCTATTTCCTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 156.4; DB 1; Pred. No. 4.3e-36; D; Mismatches 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
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US-08-554-659-1
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Patent No. 576726
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                                                                                                                         APPLICATION NUMBER: US/08/554,65
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
                                                                                            TELEFAX: (516) 742-43
TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                         ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1657 base pairs
TYPE: nucleic acid
 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Garden City
                           STRANDEDNESS:
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                                                                                                                                                                       GCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTA
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                                                                                                                                                    GTGTCACAACTGTATTGACGATGACGACGCTCATGTCGTCCACGAATGCGGCTCTGCCCA
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                                                  CTGCCTTGCTGGAGTATGC 1052
                                                                                    AGATCTCATATGTCAAGTCCATCGATGTCTATCTGGGAACTTGTTTCGTCATGGTCTTCA 1093
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Pred. No. 4.6e-36;
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; LOCATION: 27...13;
OTHER INFORMATION:
US-08-417-330A-17
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                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING TITLE OF INVENTION: GABA-A RECEPTOR AND NOVEL CLONED TITLE OF INVENTION: GABA-RECEPTOR SUBUNIT CDNA SEQUENCES NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 908-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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NAME: HAND, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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CITY: RAHWAY
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/417,330A FILING DATE: 05-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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   327
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   CTGAGTCTGAATAATTTGATGGTCAGTAAAATCTGGACGCCTGACACCTTTTTTCAGAAAT
                                 CTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAAT
                                                                     TTTTTTCGCCAGACCTGGACTGATGAGAGGTTGAAGTTTGGGGGGG---CCAACTGAGATT
                                                                                                     TTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCT
                                                                                                                                      ATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTC
                                                                                                                                                                                                          GGCTATGACAATCGGCTGCGGCCCGGGATTTGGAGGTGCTGTCACTGAAGTCAAAACAGAC
                                                                                                                                                                                                                                            GGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908-594-4720
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                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 4.7e-36;
0; Mismatches 398
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BOX 2000
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US-09-002-361-7
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Patent No. 6329516
GENERAL INFORMATION:
                                                                                                                                                                           NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite
              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            APPLICANT: Halling, TITLE OF INVENTION:
                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                     COMPUTER:
                                                                                                                      ZIP: 08543
                                                                                                                                      COUNTRY:
                                                                                                                                                        STATE:
                                                                                                                                                                        CITY: Lawrenceville
   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGGGCTGACTCTGCCCCAGTTT 708
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; NAME/KEY: Coding Sequence
; LOCATION: 2...667
; OTHER INFORMATION:
US-09-002-361-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.9%;
Best Local Similarity 54.6%;
Matches 367; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
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STRANDEDNESS: single
TOPOLOGY: line*
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
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                                                                           496
                                                                                               939 CACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGA 998
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TGTGTACCTCGGCACCTGCTTCGTTATGGTGTTCACCAGTCTGCTAGAGTACGCGACGGT
                                                                           CACGCTCATGTCTTCCACTAATGCGGCGCTGCCGAAGATCTCGTACGTTAAGTCCATCGA
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Pred. No. 1.9e-33;
0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------TCGGCTACACCATGCGGGA
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Qy 1059 AAATTTTGTTTC 1070
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Db 616 GGGGTATATGTC 627

Search completed: June 30, 2003, 23:02:26 Job time: 116 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq
   Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/U;

2: /cgn2_6/ptodata/2/pubpna/U;

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17: /cgn2_6/ptodata/2/pubpna/U;

18: /cgn2_6/ptodata/2/pubpna/U;

19: /cgn2_6/ptodata/2/pubpna/U;

10: /cgn2_6/ptodata/2/pubpna/U;
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_N
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 18 19 | c 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | . 01 | 4 | ω | 2 | | Result |
|--|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-----------------|-------------------|-------------------|-------------------|----------------|
| 152 151.6 | 153.4 | 155 | 162.6 | 162.6 | 167 | 168.6 | 171.8 | 174.2 | 181.6 | 187 | 187.6 | 193 | 219 | 480.6 | 807.8 | 1524.8 | 1640 | Score |
| 9.3 2.3 | 9.4 | 9.5 | | | | 10.3 | 10.5 | 10.6 | 11.1 | 11.4 | 11.4 | 11.8 | 13.4 | 29.3 | 49.3 | 93.0 | 100.0 | Query Match |
| 1150 455 | 569 | 480 | 1608 | 1458 | 3598 | 1467 | 3442 | 1640 | 1609 | 4621 | 1197 | 1555 | 492 | 679 | 993 | 2565 | 1640 | Length |
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| Sequence 13, Appl Sequence 5998, Ap | Sequence 19, Appl | Sequence 11304. A | Sequence 9, Appli | Sequence 11, Appl | Sequence 1, Appli | Sequence 10, Appl | ω | Sequence 12, Appl | Sequence 11, Appl | Sequence 13, Appl | Sequence 10, Appl | Sequence 11, Appl | Sequence 15843, A | | Sequence 9, Appli | Sequence 1, Appli | Sequence 3, Appli | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | <u>3</u> 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | |
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| 125.8 | 127 | 127 | 128.6 | 130.6 | 130.6 | 135.2 | 136.2 | 136.2 | 136.2 | 136.2 | 136.2 | 136.2 | 137 | 137 | 137 | 137 | 137 | 137 | 137 | 138.8 | 138.8 | 138.8 | 142.2 | 143.2 | |
| 7.7 | 7.7 | 7.7 | 7.8 | 8.0 | 8.0 | 8.2 | æ .ω | 8.3 | 8 .3 | 8 . 3 | 8.3 | 8 . u | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 8.4 | 8 .5 | 8.5 | 8.5 | 8.7 | 8.7 | |
| 2819 | 1568 | 1398 | 184 | 1866 | 1693 | 1052 | 1987 | 1422 | 1404 | 1263 | 1179 | 1038 | 3282 | 3282 | 2593 | 1323 | 1323 | 1323 | 1323 | 1272 | 1269 | 1192 | 4077 | 1997 | 1 |
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| US-09-818-657-1 | US-09-893-321-5 | US-09-893-321-1 | US-09-864-761-28002 | US-09-964-824A-96 | US-10-037-270-131 | US-09-969-844-8 | US-10-037-270-331 | US-09-742-311-1 | US-09-765-069-1 | US-09-765-069-7 | US-09-765-069-3 . | US-09-765-069-9 | US-09-825-301-75 | US-09-954-531-1034 | US-10-106-698-2031 | US-10-010-742-38 | US-09-910-689-38 | US-09-778-320-38 | US-09-510-662A-38 | US-09-808-483-7 | US-09-808-483-3 | US-09-808-483-5 | US-10-239-420-6 | US-10-037-270-256 | |
| Sequence 1, Appli | Sequence 5, Appli | Sequence 1, Appli | Sequence 28002, A | Sequence 96, Appl | Sequence, 131, App | Sequence 8, Appli | Sequence 331, App | Sequence 1, Appli | Sequence 1, Appli | Sequence 7, Appli | ω ` | Sequence 9, Appli | Sequence 75, Appl | Sequence 1034, Ap | Sequence 2031, Ap | Sequence 38, Appl | Sequence 38, Appl | Sequence 38, Appl | • | Sequence 7, Appli | Sequence 3, Appli | Sequence 5, Appli | Sequence 6, Appli | Sequence 256, App | and die an analysis |

ALIGNMENTS

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; TYPE: DNA; ORGANISM: homo sapiens; FEATURE: ; FAATURE: ; NAME/KEY: CDS; LOCATION: (1)..(1293) US-10-075-846-3
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                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1640; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
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ATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG
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RESULT 2

US-10-075-846-1

US-10-075-846-1

Sequence 1, Application US/10075846

Publication No. US20030032608A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYC

TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA-

FILE REFERENCE: D0079 NP

CURRENT APPLICATION NUMBER: US/10/075,846

CURRENT FILING DATE: 2002-02-13

PRIOR APPLICATION NUMBER: US/269,535

PRIOR APPLICATION NUMBER: US/269,535

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 1

LENGTH: 2565

TYPE: DNA

ORGANISM: homo sapiens

FEATURE:

NAME (YEV. COS
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Pred. No. 0;
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                                                                  CTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTGCCATAAATTTTGTTTCTCGTCAGCAT 1080
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                               GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC
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      CGGGCTGTCTCCCCTTTCACTTTCCTCATCATCAATATCTTCTACTGGGTTGTCTATAAA
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Sequence 9, Application US/10075846
PUBLICATION NO. US20030032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A PITTLE OF INVENTION: IN THE GASTROINTESTINAL TRAFFILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US/069,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 81
SOFTWARE: PatentIn version 3.0
SEO ID NO 9
LENGTH: 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 9
; LENGTH: 993
; TYPE: DNA
; ORGANISM: homo :
US-10-075-846-9
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US-10-075-846-9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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TA 1580
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                                                      TCTGAAGGCCCATATCTGCACCCCCCAGGACTACCGGGTGAATGTCTTCTTGCGGCAA
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; Pred. No. 1.9e
0; Mismatches
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Sequence 5, Application US/10075846

Publication No. US20030032608A1

REMERAL INFORMATION:
REPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 679
TYPE: DNA
ORGANISM: homo sapiens
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US-10-075-846-5
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                                    Matches 483;
                                                  Best Local Similarity
1118 AACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTTGG
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                                     Conservative
                                                 29.3%;
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                                     0;
                                    Score 480.6; DB 9;
Pred. No. 1.9e-146;
0; Mismatches 4;
                                                             Length
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NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.

SEQ ID NO 15843

LENGTH: 492

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(492)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15843
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US-09-918-995-15843
; Sequence 15843, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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                                                                                                                            Query Match
Best Local S
Matches 219
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SET
TITLE OF INVENTION: FROM VARIOUS cDNA LII
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                       Local Similarity
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  TCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTATGTGGGCCTATATTGCATGGTGCC
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            679
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                                                                                                                            Score 219; DB; Pred. No. 6.8: 0; Mismatches
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CDNA LIBRARIES
                                                                                                                                         DB 9; 1
6.8e-61;
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| SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-211-673-11 Query Match Best Local Similarity 53.3%; Pred. No. 4.5e-52; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 0; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 193; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 193; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 193; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 193; Mismatches 380; Indels 45; Gaps 2; Matches 486; Conservative 193; Mismat | LENGTH: 1555 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE: FATURE: LOCATION: 471402 | TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-1307 TELEFAX: 732-594-4720 TELEFAX: 702-594-4720 TELEX: <unknown> INFORMATION FOR SEO ID NO: 11: SEQUENCE CHARACTERISTICS:</unknown> | PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB95/02323 FILING DATE: 29-SEP-1995 ATTORNEY/AGENT INFORMATION: NAME: Xu, Yang REGISTRATION NUMBER: 45,243 REFERENCE/DOCKET NUMBER: T1292 | MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: FastSQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/211,673 FILING DATE: 02-Aug-2002 | DENCE ADDRESSEE: MerclesSEE: MerclesSEE: MerclesE: P.O. Bo: ET: P.O. Bo: ERAHWAY ERY: USA O7065-0900 O7065-0900 | RESULT 6 US-10-211-673-11 Sequence 11, Application US/10211673 Publication No. US20030013158A1 GENERAL INFORMATION: HORAGELES, Beatrice Whiting, Paul John TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT NUMBER OF SECTIONS: 14 | Db 177 TCCCACTCAGAACTTCAACTACCAGTCCCAAAGCTATGTGGGCCTATATTGCATGGTGCC 236 Oy 1584 AATGGTGGCTGTACTTATAAAGATGGCTTATCTACCCTA 1622 Db 237 AATGGTGGCTGTACTTATAAAGATGGCTTATCTACCCTA 275 |
|--|--|--|---|---|---|--|---|
| RESULT 7 US-10-239-420-10 Sequence 10, Application US/10239420 Fublication No. US2003099984A1 GENERAL INFORMATION: APPLICANT: Cully, Doris F. APPLICANT: Cheng, Yingcong TITLE OF INVENTION: CHANNELS ENCODING LIGAND GATED ION TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS FILE REFERENCE: 20629P CURRENT APPLICATION UNMBER: US/10/239,420 CURRENT FILING DATE: 2002-09-23 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR APPLICATION NUMBER: BCT/US01/09956 PRIOR APPLICATION NUMBER: 60/193,935 PRIOR FILING DATE: 2000-03-31 NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 4.0 | | 922 ACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCC | Oy 802 CAGATGGGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCCTGTCC 861 | Oy 682 GCTGAGGGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGT 741 | Oy 562 ATGCAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTT 621 | 111 111 111 111 111 111 1111 1111 1111 1111 | Db 287 GCCAACATGGAGTACACCATGACGGTGTTCCTGCACCAGAGCTGGCGGGACAGCAGGCTC 346 Oy 322 TCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCGATGCTGGACTCTATC 381 |

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: LENGTH: 1197
: TYPE: DNA
: ORGANISM: Rhipicephalus sanguineus
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                                                              ATGGCTGTGTGTCTTTGTGTTTCGCCTGCCTTGCTGAGTATGCTGCCATAAATTTT
                                                                                                             AGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGG
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GCCTCGCG
                                               ATATCGGGCATCAACGCCTCGCTGCCTCCCGTTTCCTACACCAAGGCCATTGACGTGTGG
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TYPE: DNA
ORGANISM: Heliothis
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RESULT 8 US-09-969-844-13

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Sequence 13, Application US/0996984

Publication No. US20020192776A1

GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Michael David Tomalski
APPLICANT: Wincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-1 072667 0.178

CURRENT APPLICATION NUMBER: US/09/969,844

CURRENT FILING DATE: 2001-10-03

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure LOCATION: (764)...(764) OTHER INFORMATION: n is
                          868
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TCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGGCCTGGGGCATCACCACCGTG
                                                                                                        GGCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTC
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                                                                             AGTTACTACCTGATCCAGATCTACATTCCGTGCTGCATGCTGGTCATCGTGTCCTGGGTG
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Pred. No. 8.2e-50;
0; Mismatches 346;
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447

569 507 629

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707 687 764 747 747

941

389 327 449

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APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Wichael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-1 072667 0178
CCURRENT APPLICATION NUMBER: US/09/969,844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
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US-09-969-844-11.
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; OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned; OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
US-09-969-844-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09969844 Publication No. US20020192776A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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TYPE: DNA
ORGANISM: Artificial
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Local Similarity 54.2%;
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                                                                                                                                                                                                                              GTGTACATCCGAATCTTCCCCAACGGCAACGTGCTGTACAGCATCCGAATCTCCCTGACG
                                                                                                                                                                                                                                                                                                                                     CCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                CCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACA 267
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                                                                                                                                                                   TTGTCCTGCCTGATGGACCTCAAGAACTTCCCCCATGGACATCCAGACGTGCACGATGCAG
                                                                                                                                                                                                                                                                                                                CCTGATCTATTCTTCCCAACGAGAAGGAAGGTCATTTCCACAACATCATCATGCCGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTAC
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  ACCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTTGCTAGTGGCTGAG
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                                                                                                     CTTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTAC
                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 349;
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Publication No. US20020192776A1

GENERAL INFORMATION:
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Wincheel David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815-I 072667.0178

CURRENT APPLICATION NUMBER: US/09/969,844

CURRENT TILING DATE: 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: PCR amplified fragment of Heliothis DNA cloned
; OTHER INFORMATION: into pCR2.1-TOPO vector (Invitrogen)
US-09-969-844-12
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US-09-969-844-12
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                Matches
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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TAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAAGTTACTGCGCATCTT 464
                                                                                                                                                                                                                            CAACATGTATCTACGGTCCATCAGCAAAATAGATGATTACAAAATGGAATACTCCGTACA 356
                                                                                                                                                                                                                                                                     CAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAA 284
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                                                                                                                                              ATTAACGTTTCGGGAACAATGGTTAGATGAACGGCTCAAATTCAATAATCTTGGAGGTCG 416
                                                                                                                                                                      TGTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGA 344
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                                                                                                 CTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGC 404
                                                            CCTCAAATACCTGACACTGACTGAAGCCAACAGAGTCTGGATGCCTGATCTATTCTTCTC
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                               10.6%;
                                                                                                                                                                                                                                                                                                           Score 174.2; DB 9;
Pred. No. 6.7e-46;
0; Mismatches 343;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1225)
US-10-239-420-3
                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-10-239-420-3
                                                                                                 PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Versio
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: CUILLY, DOTIS F.
APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DAN MOLECULES ENCODING LIGAND GATED IC
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
TILE REFERENCE: 206296
CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
                                                        TYPE: DNA ORGANISM: Dermacentor variabilis
                                                                                      LENGTH: 3442
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: Sequence 10, Application US, Patent No. US20020127199A1 ; GENERAL INFORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Zhou, Ping
                                                                         RESULT 12
US-09-815-925-10
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Best Local Similarity
Matches 454; Conserv
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GACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACC '501
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                                                                                                                       ACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCC
                                                                                                                                                                                                                                       TGGGTCTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACC
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                                                                                            ACGCTGCTCACTATTTCTTCCAAGGGCTCCGGTATACAGTCCAACTTGCCTCCGGTCTCA
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Pred. No. 6.5e-45;
0; Mismatches 357
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CURRENT APPLICATION NUMBER: US/09/815,925
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/56,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: pt_Ft_genes Version 2.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 1467
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; LOCATION: (46)..(1464)
US-09-815-925-10
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Best Local Simi
Matches 474;
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020127199A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2H
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ORGANISM: Homo sapiens
FEATURE:
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                                   769
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                                                                                                                                                                GAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAAGGGGGCTGACTCTGCCCCAGTTT
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CCTCGACTGTCACTGAGCTTTCGGTTGAAGAGGAACATTGGATACTTCATTCTTCAGACT
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                                                                                                                                                                                                                                                                                                          AAGAACTTCCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTC
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                                 ACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTCAGATG
                                                                                                      ATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGGAAATTC
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                                                                     -TCTCCATCGTGGAGCACCGTCTGGTCTCGAGGAATGTTGTCTTCGCCACAGGTGCCTAT
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Pred. No. 4.3e-44;
0; Mismatches 379;
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PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1
LENGTH: 3598
TYPE: DNA
ORGANISM: Dermacentor variabilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Matches 451;
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zheng, Yingcong
TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND GATED ION
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/239,420 CURRENT FILING DATE: 2002-09-23 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: NAME/KEY: CDS LOCATION: (170)...(1363)
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                          442 GACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACC
                                                                               382 TGGAAGCCAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACG
                                                                                                                                                       322 TCCTACCGAGAATATCCTGATGACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATC
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                                                                                                                                                                                                                      262 ACCACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTG
                                                              TGGAAACCGGAAGTATTCTTCGCAAATGCCAAACACGCAGAGTTCCAATATGTCACAGTA
                                                                                                                           ACGAGCCCCAACGTATCCAGGCCCCTGGACCTCAATGATCCAAAGCTGGTGCAGCGTATA
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Pred. No. 2.5e-43;
0; Mismatches 360
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; NAME/KEY: CDS
; LOCATION: (1)..(1455)
US-09-808-483-11
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Patent No. US20020001824A1
GENERAL INFORMATION:
APPLICANT: Bayer aktiengesellschaft
TITLE OF INVENTION: Ligand-gated anion channels
FILE REFERENCE: Lie A 3 4 397
CURRENT APPLICATION NUMBER: US/09/808,483
CURRENT FILING DATE: 2001-03-14
                                                                                                           Matches
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                    SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: DE 100 136 19.2
PRIOR FILING DATE: 2000-03-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Drosophila
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                                    GTTACGACAAGATGAGACCGCCGAAGAAGAGAGGGTCAGCCGACGATAGTCTACTTCCATG
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Pred. No. 3.9e-42;
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US-09-808-483-9
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; Sequence 9, Application US/09808483
; Patent No. US20020001824A1
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PRIOR APPLICATION NUMBER: DE 100 136 PRIOR FILING DATE: 2000-03-18 · NUMBER OF SEQ ID NOS: 18
                                                 CURRENT APPLICATION NUMBER: US/09/808,483
CURRENT FILING DATE: 2001-03-14
                                                                                 APPLICANT: Bayer Aktiengesellschaft TITLE OF INVENTION: Ligand-gated anion FILE REFERENCE: Le A 34 397
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LENGTH: 1608
TYPE: DNA
CRGANISM: Drosophila melanogaster
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1605)
US-09-808-483-9
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SEQ ID NO 9
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                            1007
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                                                                  GCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGA 1006
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Qy 1067 T 1067 b 968 T 968

Search completed: June 30, 2003, 23:06:59 Job time : 269 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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| 133 | 392 | 13483 | G40443 | 300 | M58789 | M96411 | 270 | ALEOSN | G18616 | 3634 | 25 | 2958 | 9 | 1385 | 9687 | 3061 | 9338 | BG203115 | 8616 | 6779 | 0366 | 4234 | 4459 | 65339 | C02985 | 33223 | 830 | 919 | 372 | BQ938794 | 097 | 182519 | | 173632 | 90646 | C02250 | 02709 | M4406 |
| 309 yt75d07. | 92407 pgpln.pk | 3DG111 | 04434 6024205 | 53004 6031936 | 87895 1700068 | 64113 UI-M-EQ0 | 52703 6031939 | 47390 Tetraod | 86165 RST5010 | 36340 60336004 | 29116 if1 7 g | 29587 if20e03. | 15 HSC10G061 | 913857 60318 | 196871 RST16098 | 30616 PM2-M | 93387 RST1251 | 5 RST2248 | 36166 | 5779 | 29643 | 12344 | 14592 UI-M- | 53397 BB653397 | 29850 Homo sa | 3223 AU133223 | 30621 PM2-MT | G189196 RST8236 | 13727 Mus mus | Q938794 AĞENCOU | AW280976 fj48d02 | 1825190 60 | 538200 ALS | 36322 60336002 | F906462 ILO-OT | C022502 Homo sap | C027094 Mus musc | M4 4 |

ALIGNMENTS

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM COMMENT FEATURES DEFINITION Genome Research Group National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nirs.go.jp method:uni-directional sequence direction:se (5' -> 3') Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzias.
1 (bases 1 to 662) AU169868 AU169868 Mita,K., Ishikawa,Y. and Yamauchi,M.
Establishment of cDNA database of medaka, Oryzias latipes
Unpublished (2001)
Contact: Mita K EST. Japanese medaka. AU169868 AU169868.1 sequence 662 bp mRNA linear EST 29-JAN Ol-br-ad cDNA Oryzias latipes cDNA clone br5332, mRNA Location/Qualifiers
1. .662 /organism="Oryzias latipes" /strain="HNI" GI:12591937 662 bp direction:sequenced from T3 primer EST 29-JAN-2001

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BASE COUNT
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Eukaryota; Metazoa;
         Mus musculus
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/clone="br5332"
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/sex="female/male mixed"
/tissue_type="brain"
/dev_stage="adult"
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1 (bases
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             GGTCACTGCCTCCAAATGAAAGATG----
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10437 row: g column: 01
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                               CAACGCTTGGAGGAAGATATCATCCAAGAAAGTCGTTTCTATTTCCGTGGCTATGGCTTG
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                                                                                                                                                                                                                                                                                                                                                          ACTACACAGAGTTCAGG-TTCCAGGCATCTCTGCCAAAGGTCTCCTATGTGAAAGCAATT
                                                                                                                                                                                                                                                                                                                                                                               ACCACCCAGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATC
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                                       GGCCACTGCCTGCAGGCAAGAGATGGAGGTTCCAATGGAAGGTTCTGGCATTTATAGTCCC
                                                                                    CAGAATAAGGAAGATGTTACTCGTGAAAGTCGTTTTAACTTCAGTGGCTATGGGATG
                                                                                                                                                                           GTGAA-CTTGTCTCCAGGCAACATAAGGAGTTCCTTCGTCTCCGGAGACGACAGAAGAGG
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(bases 1 to 817)
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/lab_host="NH10B (phage-resistant)"
/lab_host="NH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Note: taize 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."

a 190 c 192 g 212 t
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/clone="IMAGE:4527768"
/clone_lib="NIH_MGC_94"
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            264 CACAATGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTC
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Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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AV729257 HTC Homo sapiens cDNA clone
AV729257
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1 (bases 1 to 678)
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                                                                      CCCACCGGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGAC
                                                                                                               GGACAAGTTAATGGGAAGGACATCAGGATATGATGCAAGAATCAGGCCAAATTTTAAAAGG
                                                                                                                              AGACAAACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGG
                                                                                                                                                                                                  AAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCCCATGTCCCCCCTCTGATTTCCT
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                                                                                                                                                                      AGACCATGACTCCAGGTCTGGAAAACAACCTTCACAGACCCTATCTCCTTCAGATTTCTT
GACCATGGACTACCGAGTGAATATTTTTCTGAGACAACAGTGGAATGATTCACGGCTGGC
                                                       TCCTCCAGTAAACGTTACTTGCAATATTTTTATCAACAGTTTTGGATCAGTCACAGAAAC
                                                                                                                                                                                                                                                                                                      199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l: hanzg@chgc.sh.cn
clone is available at CHGC in
                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCCHE03"
/clone_lib="HTC"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Hypothalamus"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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74.9%;
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Pred. No. 4.3e-52;
0; Mismatches 124;
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Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Musculus (Labace) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779) (1.779)
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Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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http://image.llnl.gov
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Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 692)
Bonaldo,M.F., Lennon,G. and So
                                                                         6001 Executive Blvd.
20892-9643, USA
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                                                                                                             Contact:
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clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The tissue for this library was contributed by Dr. Xin-Yuan Fu,
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/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DBH10B (Life Technologies)"
/lab_host="DBH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.ulowa.edu. The tissue
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159 c 144 g
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/db_xref="taxon:10090"
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0; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAS whose availability will be considered under appropriate and limited collaborative arrangements The tissue for this library was contributed by Dr. Xin-Yuan Fu, vale University School of Medicine Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-M-CG0p-bdc-d-08-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CG0p-bdc-d-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 443 1706
Fax: 301 443 9890
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                  AAGGCCCACCCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCA
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/db_xref="taxon:10090"
/clone="UI-M-CGOp-bdc-d-08-0-UI"
/clone_1ib="NIH_BMAP_Ret4_S2"
/lab_host="DHJ08 (Life Technologies)"
/lab_host="DHJ08 (Life Technologies)"
/note="vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_SEQ=None
162 c
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/strain="C57BL/6J"
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Pred. No. 1.3e
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Cogburn, L.A. and Nys, Y.
ESTs from Normalized Chicken Reproductive Tract cDNA library-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-135
Fax: 302-831-2822
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Contact: Larry A.
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       Conservative
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Location/Qualifiers
                                                                                                                                                                         /note-"Vector: pcmySport6; Library made from three total RNA pools from each tissue (testis 25%, ovary 25%, and ovidut 50% of final RNA pool); Single pass sequencing from 5'-end"
198 c 181 g 88 t
                                                                                                                                                                                                                                                                                                                                                              and sexually-mature"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Normalized Chicken Reproductive Tract cDNA Library (pgrln)"
/sex="Male and Female"
/tissue_type="Testis, ovary and oviduct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Commercial broiler
/db_xref="taxon:9031"
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Score 239.6; DB 13;
Pred. No. 2.7e-40;
0; Mismatches 89;
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Mus musci
                                                               Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAK Plate: 54 Row: 1 Column: 1
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 1
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                         USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (04-APR-2002) National Institutes of Health
Submitted (04-APR-2002) National Institutes Office, Nation
Gene Collection (MGC), Cancer Genomics Office, Nation
Institute, 31 Center Drive, Room 11A03, Bethesda, MD
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Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5360070"
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IMAGE:5360070,
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502; Conser
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                                                                                                                          GATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCGTGAACGTGACCTGCAACA
                                                                                                                                                                                                                                                                                                                                                                       AATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGCTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAATGAAAAAAGTGCCAATTTTCATGATGTGACCCAAGAAAATATCCTGTTGTTTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTGCGGCAACAGTGGAATGACCCACGCCT-GTCCTACCGAGAATATCCTGA----TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCT
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                                                                                                                                                                                                                   TGGATGCTGCCCCTGTGGGGCCTGGGGCATCACCACCGTGCTCACCATGACCACCCC
                                                                                                                                                                                                                                                                       GCGTATATGCACCAACCTTGCTGATTGTGGTTCTCTCCTGGCTCTCTTTCTGGATCAACC
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                                                        GGCTCATTGCCTGCTCTTCGGGTTTGCCTCCTCGTGGAGTACGCTG
                                                                                             GGATGGCTGTGTCTCCTCTTTGTGTTCGCTGCCTTGCTGGAGTATGCTG
                                                                                                                                                                                                 CTGATGCTAGTGCTGCCAGAGTACCTCTGGGCATCTTCTCCGTGCTCAGTTTGGCCTCAG
                                                                                                                                                                                                                                                                                         AGATGTACATCCCCAGCCTACTCATCCTCATCCTGTCCTGGGTCTCCTTCTGGGATCAACA 883
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587 c 607 g 920 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Eye, retina,/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
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   537
                                                                      477
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                                  404
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                                                                                                                                                                                                                                                                                                                                                   502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 32 Row: b Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504022 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2390,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
BC022502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC022502.1 GI:18490294
                                                                                                                                                                                                           TTTTTATTAACAGTTTTGGATCCATTCAAGAAACAACAATGGACTATAGAGTTAACATCT
                                                                                                                                                                                                                                      TCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCT
                                                                                                                                                                                                                                                                            GTTATGATCCCAGGATAAGACCAAACTTCAAAGGCATTCCTGTTGATGTAGTAGTCAACA
                                                                                                                                                                                                                                                                                                    GATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCACCCGTGAACGTGACCTGCAACA
CTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCT
                                                                                       ACTCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCCTCTTCTTG
                                                                                                                                                                        TCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACCGAGAATAT-----CCTGATG
                                                                   TCCTGAGACAAAAATGGAATGACCCCAGGTTGAAGCTCCCCAGTGATTTTAGGGGTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
/note="Vector: pB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="LocusID:2743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Brain, hypothalamus"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4792516"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
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56.3%;
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Primates;
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Pred. No. 4.3e-36;
0; Mismatches 340;
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MAGE:4792516, mRNA.
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GCCTTATTGCCTTCCCTTTTGGGTTTGCCTTCCCTGGTGGAGTATGCAG
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                                                                                        AGTGCACAACCCTTGCCGCTGAGCTTCCCAAAGTTTCCTATGTGAAGGCTCTTGATGTTT
                                                                                                                                       AGAGCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCT 1003
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SOURCE ORGANISM REFERENCE KEYWORDS JOURNAL MEDLINE TITLE AUTHORS EST

LOCUS
DEFINITION
ACCESSION

BF906462 ILO-OT0123-081200-500-a09

536 bp mRNA lir OT0123 Homo sapiens

linear CDNA,

mRNA sequence. EST 18-JAN-2001 BF906462/c

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VERSION

BF906462.1 BF906462

GI:12297920

COMMENT Laboratory of Cancer Genetics Ludwig Institute for Cancer Re Rua Prof. Antonio Prudente 10 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Tel: +55-11-2704922 Fax: +55-11-2707001 Brazi Contact: Simpson A.J.G. Proc. Natl. sequence tags Shotgun sequencing Simpson, A.J (bases 1 to 536) Acad. Sci. of the human transcriptome with ORF U.S.A. er Research e 109, 4 and 97 (7), andar, 01509-010, Sao Paulo-SP,

Email: asimpson@ludwig

This sequence was

derived

from

the

FAPESP/LICR Human

Cancer Genome

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Seq primer: puc 18 forward
High quality sequence stop: 518.
               Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 762)
NIH-MGC http://mgc.nci.nih.gov
                                                                                                                                                                                              BI736322 76
603360026F1 NIH_MGC_94 Mus
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National Institutes of Health, N
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/clone_lib="OT0123"
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pred. No. 3e-35;
0; Mismatches 144;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11934 row: c column: 08
                                                              AL538200
AL538200 LTI_FL013_FBrn1
                                prime, mRNA
AL538200
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                 AL538200.1
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/db xref="taxon:10990"

/clone="IMAGE:5367103"

/clone_1lb="NHH_MGC_94"

/tissue_type="retina"

/tissue_type="retina"

/lab_host="DH10B (phage-resistant)"

/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1;

/site_2: Sal1; Cloned unidirectionally; Oligo-dT primed.

Average insert size 3.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

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Unpublished (2001)
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GGGGTCTACGCCCCAACCCTGCTCATTGTTGTTCTCTCTGGCTTTCCTTCTGGATCAAC
                         CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGGGTCTCCTTCTGGATCAAC
                                                     AACAAMAMADDBKTKGTAGTCATCTTCACCCTGAGGAGGCAGGTCGGCTTTTACATGATG
                                                                              AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT
                                                                                                           GATATCAAAAAGGAAGATATTGAATATGGTAACTGTACAAAATACTATAAAGGCACGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockvill, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uccb:
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/dev_Stage="pooled tissue from
week, 24 week and 26 week)"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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nes 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM11407 row: e column:
High quality sequence stop: 844.
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Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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  TGAATATCCTGACGACTCTTTAGACCTCGACCCCTCCATGTTGGACTCCATTTGGAAACC
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                                                                                                                                                                                                                                                                                                                                                        /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RAR source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note this is a NIH_MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5164025"
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/lab_host="DH10B"
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Pred. No. 6e-26;
0; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest 180
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTs: fj48d02.x1
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Actinopterygii; Neopterygii; Teleostei;
; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alab (web address: www.resgen.com) (email contact: info@resgen.com) RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: John Ngai. cDNA Library Arrayed
Matthew Clark. DNA Sequencing by: Washington University Go
Sequencing Center Clone distribution: Genome Systems, St
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Location/Qualifiers
                                                                                       /lab_hosi""E. coli DH10B"
/note""Vector: pzIPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdazIPLOX. N
excision of the cDNA library was performed to yield
                                           pZIPLOX plasmids. Insert check was library."
                                                                                                                                                                                   /sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                       /clone_lib="zebrafish adult brain"
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/db_xref="taxon:7955"
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Ostariophysi; Cypriniformes
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471 GTCCATGCTGGACTCCATCTGGAAACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13990 row: P column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 975)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5', mRNA sequence
BQ938794
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AGENCOURT_8930535 NIH_MGC_94
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                                                                                            /db_xref="taxon:10000"
/db_xref="taxon:10090"
/clone="nMAGE:646631"
/clone="lib="NHLMGC_94"
/tlssue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
63 a. 234 c 221 g 257 t
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Pred. No. 2.4e-25;
Pred. No. 2.4e-25;
                    Score 159.6;
Pred. No. 1.6
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299 -----TTGGATATACAACCGATGATTTA 321
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                                                                                                                            883 ATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCATGACCACC
                                                                                                                                                                                     823 CAGATGTACATCCCCAGCCTAACTCATCCTGATCCTGTGCTGCGTCTCCTTCTGGATCAAC
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                                                                                                                                                                                                                                                                                   382 GATATTAAAAAGGAGGATATCGAATATGGCAACTGTACAAAATACTATAAAGGCACTGGT 441
                                                                                                                                                                                                                                                                                                                                          322 AGATTCATCTGGCAGTCAGGAGATCCTGTTCAGTTGGAAAAAATTGCTTTACCTCAATTT 381
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                                                                                                              562 CCTGATGCTAGTGCCAGAGTACCTCTGGGCATCTTCTCCGTGCTCAGTTTGGCCTCA
                                                                                                                                                                                                                                              763 AAATTCACCTGCATCGAGGTAAAGTTTCACCTGGAACGGCAGATGGGCTACTATCTGATT 822
                                                                                                                                                                                                                                                                                                      703 CAGTITATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGCACTACAACACAGGG
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AAE21178 ABB19336 ABB19337 AAE13037 AAE13038 AAE16395 AAE16395 AAE13312 AAE13311

Human TRICH-22 pro
Amino acid sequenc
Mouse ischaemic co
R. sanguineus glut
R. sanguineus glut
R. sanguineus glut
Heliothis virescen
Heliothis virescen
Dermacentor variab

Domain Protein .

/label= Signal_peptide
29.417
/note= "Mature human TRICH-22 protein"
44.341
/note= "Neurotransmitter-gated ion channel domain"
172..186

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|------------------|------------|--|-----------|----------|-----------|-------------------------|------------|------------|--|-----------|----------------------|---------------|--|--------------------|---------------------------------------|--------------------|----------------------|----------------------|--------------------|--------------------|--------------------|--------------------|--|----------|----------|----------|----------|--------------------|---------------|--------------------|
| Key Pept | Homo | Human amyo card depracell cell Alzh myas acqu endo card epil | Human | 01- | AAE | SULT 1 E21178 AAE | | 45 | 44 | 42 | 410 | 39 | 38 | 36 | ω ω 4 τ | 33 | ب س بہ | 3 2 0 9 | 28 | 26 27 | 25 | 23 | 22 | 20 | 0 00 | 17 | 1 1 5 | 14 | 12 | 11 |
| tide | no sapiens | Human; trans amyotrophic cardiac disc depression; cell prolife Alzheimer's myasthenia g acquired imm endocrine di cardiac myor epilepsy; me muscle disor | an TRICH- | JUL-2002 | AAE21178; | 21178 s | | 670.5 | 673 | 678.5 | 690 | 692 | 698.5 | 704 | 712 712 | 715 | 717 | 718 717 | 719 | 720 719 5 | 720 | 720 | 724.5 720 | 724.5 | 724.5 | 725.5 | 726 | 729 | 731 | 731.5 |
| s:15 | ns. | phic latera disorder; ion; schizo oliferated er's diseas nia gravis; nia gravis; d immune de ne disorder myopathy; y; mental d disorder; s | 22 | (firs | | tandard; | - | 9. | 9. | .0 | 00 | 0 | o :- | : | | · :- : | 31.8 | | - 1 | - 2 | 2. | ı, | 2 2 | 2 | ı ک | 2. | | | 32.5 | |
| Location, 128 | | r and ior al sclerc polymyos pohrenia, disorder se; Parki ; multipl eficiency r; autoin amnesia; disorder; stroke; c | protein. | t entry | | Prote | | \vdash | ထပ | 5 | | 7 | 77 | ιω - | 7 | 9 | 496 | စယ | 9 | лω | ω c | 000 | 8 9 | 8 | ע ע | 0.0 | nω | 0 u | 537 | 455 |
| /Qua | | on cositositositositositositositositositosit | | y) | | in; | | 17 | 17 | 17 | 222 | 23 | 22 | 14 | 14 15 | 22 | 20 | 21 17 | 22 | 3 2 3 | 21 | 19 | 20 19 | 20 | 20 | 22 | 21 | 22 | 23 | 20 |
| /Qualifiers | | Human; transporter and ion channel; TRICH-22; transport disorder amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular cardiac disorder; polymyositis; diabetes; neurological disorder depression; schizophrenia; anaemia; Wilson's disease; Cushing's cell proliferated disorder; infertility; arteriosclerosis; generalizhemer's disease; Parkinson's disease; Huntington's disease myasthenia gravis; multiple sclerosis; metabolic disorder; hypoactyried immune deficiency syndrome; immunological disorder; sendocrine disorder; autoimmune thyroiditis; rheumatoid arthrit cardiac myopathy; amnosia; toxic myopathy; Addison's disease; epilepsy; mental disorder; myocarditis; Crohn's disease; Grave muscle disorder; stroke; dementia; anxiety; AIDS; asthma; cirri | | | | 417 AA. | ALIGNMENTS | AAR88360 | AAU81289 AAR88361 | AAR97299 | AAE00861 AAE00862 | ABB57078 | AAM40884 AAM39098 | AAR34035 | AAR31188 AAR59866 | ABB66256 | AAW86161 AAW97413 | AAY51076 AAR89336 | AAE13034 | AAY51075 | AAY51074 | AAW69286 | AAW81633 AAW69285 | AAW81635 | AAW81636 | AAE00864 | AAY51077 | ABB65121 | AAE13313 | AAW97860 |
| | | port disorder; angina; romuscular disorder; cancer; can disorder; cancer; e; Cushing's disease; erosis; gene therapy; sorder; hypertension; disorder; scleroderma; oid arthritis; goitre; s disease; infection; ease; Grave's disease; sthma; cirrhosis. | | | ę | | | norhabditi | Mutant gamma-amino Caenorhabditis ele | an GABA-A | form of S. | e ischaemic c | Human polypeptide Human polypeptide | Sequence of a GABA | GABA-A receptor be Human GABA recepto | Drosophila melanog | Insect GABA recept | D. melanogaster GA | Dermacentor variab | D. melanogaster GA | D. melanogaster po | GABA gated chlorid | GABA-gated chlorid GABA gated chlorid | ated | ja ted | form | nulan | Drosophila melanog | rmacentor var | Cat flea glutamate |

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sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis, myocratitis, prostate cancer, cardiac disorders associated with transport e.g. polymyositis, bradyarrythmia, dermatomyositis, angina, neurological disorders associated with transport e.g. amnesia, bipolar disorder, depression, Tourette's disorder, schizophrenia, other disorders associated with transport e.g. annesia, bipolar disorder disorders, infertility, hyperglycaemia, hypoglycaemia, wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
                                                                                                                                                                                                                    periodic paralysis, mental disorders including mood, anxiety; and immunological disorders include acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis, Grave's disease, glomerulonephrittis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, uveitis, viral, bacterial, fungal, parasitic, protozoal, haemodialysis, uveitis, viral, bacterial, fungal, parasitic, protozoal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia, goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell proliferated disorders include cancer, actinic keratosis, cirrhosis, arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis. Neurological disorders include Alzheimer's, Pick's and Parkinson's disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's disease, multiple sclerosis, dementia and other extrapyramidal disorder, motor neuron disorder, prion disease, metabolic disease of the nervous system and other developmental disorders of the central nervous system, neuromuscular disorders, metabolic, endocrine and toxic myopathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designated TRICH and nucleic acid molecules encoding such polypeptides TRICH sequences are useful for diagnosis, treatment and prevention of transport, muscle, neurological, immunological and cell proliferative disorders. Transport disorders include akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular districts of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang J, Yao MG, Lal P, Walla NK, Gandhi AR, Hafalia AJĀ;
Nguyen DB, Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y;
Reddy R, Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL;
Greene BD, Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA;
Ding L, Das D, Kallick DA, Khan FA, Seilhamer JJ;
                                       myopathy, myocarditis, polymyositis, arrhythmias and hypertension. TRICH polynucleotides are used in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human transporter and ion channel polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 66; Page 181-182; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human transporters and ion channels polypeptides and polynucleotides for diagnosing, preventing or treating transport, neurological, muscle, immunological and cell proliferative disorders
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10-AUG-2000;
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25-AUG-2000;
                                                                                                                                                                     helminthic infections and trauma; and muscle disorders include cardiac
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2000US-224456P.
2000US-226410P.
2000US-228140P.
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2000US-231434P.
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K, Gandhi AR,
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Best Local S
Matches 416
         Claim
                                        Novel nucleic acid sequence encoding human ataxia protein for compounds useful for treating disorders relating to mutations
                                                                             N-PSDB;
                                                                                                                                                                                                                                                                            Human; ataxia; gene therapy
                                                                                                                                                                                                                                                                                                                                                                      AAB19336
                                                                                                             Rappold-Hoerbrand
                                                                                                                                    (RAPP/) RAPPOLD-HOERBRAND G
                                                                                                                                                                                  23-MAR-2000; 2000WO-EP02600
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                                                                                                                                                                                                                                                                                                  Amino acid sequence of a human ataxia protein
                                                                                      2000-656166/63
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        10; Page 20-21; 47pp; English
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                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB57052 standard;
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                                                                                                                                                                                                                                                                                                                                                                         vasospastic ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse ischaemic condition related protein sequence
                                                                       (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
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5.7e-216;
nes 2;
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                            Ishii Y;
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                               Brown dog tick; glutamate-gated chloride channel; GluCl2; crop protection; insecticide; nematocide;
                                                                                                                      R. sanguineus
                                                                                                                                                                                 28-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SITLSCPLDLTLFPMDTQRCKMQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLVEYAVVQVMLNNPK - - - RVEAEKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALLEYAAINFVSRQHKEFIRLRRRQRR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LL----VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                   glutamate-gated chloride channel 1 protein, T32
                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.7%;
                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 871; DB 2
Pred. No. 1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SFGYTTDDLRFIWQSGDP-VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                     acaricide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMSPSDFLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226
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The invention relates to Rhipicephalus sanguineus (brown dog tick)
L-glutamate-gated chloride channel proteins (GluCl and GluCl2)
and nucleic acid molecules encoding such proteins. GluCl channel
proteins are useful for identifying modulators. The compounds
identified as modulators are useful for insecticidal, mitacidal
and/or nematocidal treatment for use in animal and human health
and/or crop protection. The compounds are also useful in screening
for and selecting compounds active against parasitic invertebrate
species relevant to animal and human health, including worms,
fleas, ticks, mites and lice. Heterologous cell lines expressing
functional GluCl1 and GluCl2 channel functional forms are useful
GluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluCll protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200174838-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warmke JW, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
    350
                                                                                             290
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                                                                                                                                                                                                                                                                                   187
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                                                                                                                                        275
                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                       156. KNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLV
                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD21397
                                                                                                                QMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDI
WTGVCLTFVFGALLEFALVNYASRSDSRRQNMQKQKQRKWELEPPLDSDHLEDGATTFAM
                                           WMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRRQRRQ----RLEEDIIQESRFYFRG
                                                                                        QIYIPCCMLVIVSWVSFWLDPTSIPARVSLGVTTLLTMATQISGINASLPPVSYTKAIDV
                                                                                                                                                                                   FLWKEGDP-VQVTKNLHLPRFTLERFQTDY--CTSRTNTGEYSCLRVDLVFKREFSYYLI
                                                                                                                                                                                                                     FEWLEDAPAVQVAEGLTLPQFIL-RDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLI
                                                                                                                                                                                                                                                                              PNGDVLFSIRISLVLSCPMNLKFYPLDKQICSI------VMVSYGYTTEDLV
                                                                                                                                                                                                                                                                                                                                                                                                                  VFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAIEKRILDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPMSPSDFLDKLMGRTSGYDARIRP----NFKGPPVNVTCNIFINSFSSVTKTTMDYRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPLVALAFFLLILLSCPSAWAETLPTPPTRGQGGVPVAAAMLLGKQQSSRYQDKEG-KAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VP-ATLSFLLL-----W--TLP-----GQVLLRVALA-----KEEVKSGTKGS
                                                                                                                                                                                                                                                                                                                                                                       MTFREQWRDERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-193934P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 754.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                      334
                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
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                                                                                                                                                                                      289
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Вр 20 Db Qy

Matches

157;

Conservative

61;

110;

Indels

29;

Gaps

Similarity

42 48

DPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS DERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIHPNGDVLFS

159 163 99

LDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQMTFREQWR

LDKLMGRTSGYDARIRP----NFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN 103

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RESULT 5
AAE13037
                                                                       XPPP
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XX
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                   Query Match
Best Local
                                                                                                                 and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, fleas, ticks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful for establishing functional or binding assays to identify novel gluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                     The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health and/or nematocidal treatment for use in animal and human health
                                                                     Sequence
                                                                                                       GluCl1 protein, T12.
                                                                                                                                                                                                                                                                                                                                                                                                              Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                              Claim 26; Fig
                                                                                                                                                                                                                                                                                                                                                                                                  acaricides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662963/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-193934P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhipicephalus sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluCl2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown dog tick;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE13037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE13037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2001; 2001WO-US09905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C12; crop protection; insecticide; nematocide; acaricide; protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 YGLGHCLQARDGGPMEGSGIYS---PQPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD21395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSSG------EPAGLMARTWPPPPLP
                                                                       450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                              2; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate-gated chloride channel 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glutamate-gated chloride channel; GluCl1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                   33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cully DF,
                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450
Score 742.5; DB:
Pred. No. 2.2e-68
1; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamelin MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429
                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein,
                                 Length 450;
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RRESULT 6
RAP13038
ID AAP13
XX
AAP13038
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Query Match
                                                                                                                                                                                                                                                   The invention relates to Rhipicephalus sanguineus (brown dog tick) L-glutamate-gated chloride channel proteins (GluCl1 and GluCl2) and nucleic acid molecules encoding such proteins. GluCl channel proteins are useful for identifying modulators. The compounds identified as modulators are useful for insecticidal, mitacidal and/or nematocidal treatment for use in animal and human health and/or crop protection. The compounds are also useful in screening for and selecting compounds active against parasitic invertebrate species relevant to animal and human health, including worms, flore as the parasitic modulation and human health, including worms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown dog tic
GluCl2; crop
                                                         Sequence
                                                                                                               GluCl1 protein, T82.
                                                                                                                                       species relevant to animal and human health, including worms, fleas, tlcks, mites and lice. Heterologous cell lines expressing functional GluCl1 and GluCl2 channel functional forms are useful for establishing functional or binding assays to identify novel gluCl channel modulators. The present sequence is R. sanguineus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Fig 4; 89pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel L-glutamate-gated chloride channel proteins from Rhipicephalus sanguineus for identifying compounds which modulate the channel proteins, which are useful as insecticides, anthelmintics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Warmke JW, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-193934P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R. sanguineus glutamate-gated chloride channel 1 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE13038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acaricides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFGALLEFALVNYASRSDSRRQNMQKQKQRKWELEPPLDSDHLEDGATTFAMRPLVH
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protection; insecticide; nematocide;
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acaricide;
Length
450;
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RESULT 7
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Matches 157; Conserv
New nucleic acid encoding lepidopteran chloride screening agents for insecticidal activity -
                                WPI; 2002-121133/16.
N-PSDB; AAD26939.
                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                       (AVET ) AVENTIS CROPSCIENCE SA
                                                                                                                                    13-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                  Lepidopteran glutamate-gated
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                                                                                                              13-JUN-2000; 2000US-0592891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 DPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 LDSIIGQ-GRYDCRIRPMGINNTDGPAL-VRVNIFVRSIGRIDDVTMEYTVQMTFREQWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVQVAEGLTLPQFIL-RDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFGALLEFALVNYASRSDSRRQNMQKQKQRKWELEPPLDSDHLEDGATTFAMRPLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFAALLEYAAINFVSRQHKEFIRLRRRQRRQ-----RLEEDIIQESRFYFRGYGLGH 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVIVSWVSFWLDPTSIPARVSLGVTTLLTMATQISGINASLPPVSYTKAIDVWTGVCLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRISLVLSCPMNLKFYPLDKQICSI-----VMVSYGYTTEDLVFLWKEGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DERLQYDDLGGQVRYLTLTEPDKLWKPDLFFSNEKEGHFHNIIMPNVLLRIHPNGDVLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - VQVTKNLHLPRFTLERFQTDY - - CTSRTNTGEYSCLRVDLVFKREFSYYLIQIYIPCCM
                                                                   Sarda
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                                                                                                                                    2000US-0592891
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327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.08;
                                                                   Tomalski MD,
                                                                                                                                                                                                                                                                                           "Encoded by
                                                                                                                                                                                                                                                                                                                "Encoded by TTGGTGTTGTTA"
                                                                                                                                                                                                                                              "Encoded by
                                                                                                                                                                                                    "Encoded by
                                                                                                                                                                                                                                                                   "Encoded by TCA'
                                                                                                                                                                                                                         "Encoded by
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1; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                     chloride channel;
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                                                                                                                                                                                                                          GCG"
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                                                                 Wingate
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                                                                                                                                                                                                                                                                                                                                                                                     insecticide
            channel,
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamate-gated chloride channel.

Note: This sequence SEQ.ID.NO.14 is stated to be similar to the sequence shown in the sequence listing. However this sequence lacks N-terminal six residues of the sequence shown in sequence listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific-binding or functional assays for identifying potential insectlicides. The present sequence is Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutamate-gated chloride channel. Glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of
    Misc-difference
                      Misc-difference
                                           Misc-difference
                                                               Misc-difference
                                                                                   Misc-difference
                                                                                                       Misc-difference
                                                                                                                                      Heliothis virescens
                                                                                                                                                          Lepidopteran
                                                                                                                                                                                Heliothis virescens
                                                                                                                                                                                                     09-APR-2002
                                                                                                                                                                                                                         AAE16439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                SYTKAIDVWTGVCLTFVFGALLESRFVNYASRSDMHRENMKKARRE
                                                                                                                                                                                                                                                                                                                SYVKAIDIWMAVCLLFVFAALLEYAAINFVSR--QHKEFIRLRRRQ
                                                                                                                                                                                                                                                                                                                                     REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
                                                                                                                                                                                                                                                                                                                                                                              GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
                                                                                                                                                                                                                                                                                                                                                                                                 GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFTCIEVKFHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNKLLRIFKNGNYLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVWMPDLFFSNEKEGHFHNIIM 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECMNGGKINFREKEKQILDQILG-PGRYDARIRPSGINGTDGPAVVSVNIFVRSISKIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNIFINSFSSVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Column
                                                                                                                                                                                                                                                                                                                                                         RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV
                                                                                                                                                                                                                                                                                                                                                                                                                       PNVYIRIFPNGNVLYSIRISLTLSCPMNLKLYPLDKQTCSLRM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 AA;
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                                                                                                                                                          glutamate-gated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates
                                          /note=
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                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                               glutamate-gated chloride channel, alternative
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Pred. No. 8.2e-68;
3; Mismatches 111.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamate-gated chloride channel. Glutamate-gated chloride channels are a family of ligand-gated chloride channels unique to invertebrates. The DNA of the invention is used for recombinant production of lepidopteran glutamate-gated chloride channel and this is used, optionally in the form of membrane preparations or recombinant cells, in specific binding or functional assays for identifying potential insecticides. The present sequence is Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding lepidopteran chloride channel, useful screening agents for insecticidal activity -
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                                    SYVKAIDIWMAVCLLEVEAALLEYAAINEVSR--QHKEFIRLRRRQ
                                                                                                 RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV
                                                                                                                                                              GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
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                                                                                                                                                                                                                                                                                                                                   VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVMMPDLFFSNEKEGHFHNIIM
                                                                                                                                                                                                                                                                                                                                                               TTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTT
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SYTKAIDVWTGVCLTFVFGALLESRFVNYASRSDMHRENMKKARRE
                                                                              REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
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3; Mismatches
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Pred. No. 8.3e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GABA-gated chloride channel proteins. GABA-gated chloride channel proteins exert toxic effects on other ticks or related parasites such as mites. The present sequence is Dermacentor variabilis clone 8 GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gamma-aminobutyric acid; GABA; tick infestation; mite; antiparasitic; GABA-gated chloride channel; recombinant expression; domestic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chloride channel protein.
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                                                                                                 PQFKVLGHVQKAKEVALTTGNYS--RLVC-EIRF--ARSMGYYLIQIYIPAGLIVVISWV
                                                                                                                            PQF----ILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWV
                                                                                                                                                                                                                                                      -DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILISCL 173
                                                                                                                                                                                                                                                                                                     TRGYDRRVRPNYGGVPVEVGVTMQIISISTVSEVQMDFTSDFYFRQSWRDERLSFQKSPD
                                                                                                                                                                                                                                                                                                                                     TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD 114
YAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGI
                                 SFWLHRDASPARVALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFTALLE
                                                                SFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLE
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Pred. No. 1.4e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to gamma-aminobutyric acid (GABA)-gated chichannels and their corresponding nucleic acid molecules. GABA-gate chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, deer, or other wild or domesticated animals. The nucleic acids as hybridisation probes or Polymerase Chain Reaction primers for the first process of Polymerase Chain Reaction primers for the state of the state 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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N-PSDB; AAD22072.
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nes 157; Conserv
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                                                                                                                                                                                                                                                      TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD 114
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Pred. No. 3.6e-67;
B; Mismatches 111;
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AAX24372). The invention also provides expression vectors, host cells and methods for recombinant production of CfGluCl-1. Also claimed is a method of identifying a compound that modulates GluCl protein activity which comprises: (a) injecting into a host cell solution a population of nucleic acid molecules (NAMS), at least a portion of which encodes a GluCl protein, such that expression of the portion of NAMS results in an active GluCl; (b) adding a test compound into the solution; and (c) measuring host cell membrane current at a holding potential more positive than the reversal potential for chloride. The products and methods can be used to identify GluCl channel modulators which interfere with
                                                                                                                                                                                                                                                                                                                                   This is the full-length amino acid sequence of CfGluCl-1, a new glutamate gated chloride channel of cat flea (Ctenocephalides felis). The sequence was deduced from an isolated CfGluCl-1 cDNA (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated glutamate gated chloride channels - obtained from Ctenocephalides felis, used to develop products for use against parasites, insects, aphids or nematodes
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N-PSDB; AAX24372.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tribolium sp. and Tenebrio sp., and against immature stages of insects living on plant tissue. The compounds are also useful as nematodicides for the control of soil nematodes and plant parasity such as Meloidogyne sp. The products can also be used for the production of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparasitic agents and insecticides in human and animal health and crop protection. They can be used against e.g. gastrointestinal parasites of the genera Ancylostoma, Necator, Ascaris, Strongyloides, Trichinella, Capillaria, Trichuris or Enterobius, endoparasites e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                extraintestinal stages of the intestinal worms Strongyloides and Trichinella, and ectoparasites such as ticks, fleas, mites, or l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the filarial worms Wucheria,
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                                                                            300
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360 SLD 362
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                                                                                                                                                        EED 378
                                                                            GINASLPPVSYTKAIDVWTGVCLTFVFGALLEFALVNYASRSDMHRENMKKKRRELEQAA
                                                                                                                GSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINEVSR--QHKEFIRLRRRQRRQRL
                                                                                                                                                                                                 CIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSS
                                                                                                                                                                                                                                                                                                                                                              GANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCS
                                                                                                                                                                                                                                                                                                                                                                                                      LRSISEIDDYKMEYSVQLTFREQWQDERLKFNDFGGRLKYLTLTEASRVWMPDLFFANEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPN----FKGPPVNVTCNIF
                                                                                                                                                                                                                                         ----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYS
                                                                                                                                                                                                                                                                             PLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFT
                                                                                                                                                                                                                                                                                                                          EGHFHNIIMPNVYIRIFPYGSVLYSIRISLTLACPMNLKLYPLDRQVCSLRM------
                                                                                                                                                                                                                                                                                                                                                                                                                                            INSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLGGGKENFRAKEK-----QVLDQILG-PGHYDARIRPSGVNGTGDGPTV-VAVNIY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The GluCl channel modulators can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 731.5; DB 20; Pred. No. 3.2e-67; 0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brugia, or Onchocerca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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RESULT 12 ·
AAE13313
                       AAE13313 standard;
AAE13313;
                        Protein;
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Dermacentor variabilis clone 9 12-FEB-2002 (first entry)

Gamma-aminobutyric acid; GABA
GABA-gated chloride channel; acid; GABA; tick infestation; mite; antiparasitic; recombinant expression; GABA-gated chloride channel protein. domestic

Dermacentor variabilis

PD XXX PD XXX

WO200174884-A1

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RESULT 13
AAW05246
ID AAW05
XX
AC AAW05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to gamma-aminobutyric acid (GABA)-gated chloride channels and their corresponding nucleic acid molecules. GABA-gated chloride channel proteins and DNA's are useful for preventing and treating tick infestation, particularly in humans, dogs, cattle, horses, deer, or other wild or domesticated animals. The nucleic acids are useful as hybridisation probes or Polymerase chains Reaction primers for identifying the presence of Dermacentor variabilis GABA-gated chloride channel nucleic acid or DNA's encoding for a GABA receptor. The nucleic acids are also useful for the recombinant expression of D. variabilis GABA-gated chloride channel proteins. GABA-gated chloride channel proteins acids or related parasites such as mites. The present sequence is Dermacentor variabilis clone 9 GABA-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide useful for preventing or treating tick infestation, in humans, dogs, cattle, horses, deer, or other wild or domesticated animals, comprises the Dermacentor variabilis gamma-aminobutyric acid (GABA)-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chloride channel protein.
   AAW05246
                                AAW05246 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD
                                                                                                                                                          YSPQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 1; 59pp; English.
                                                                                                                                                                                                                                                              SFWLHRNASPARVALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFTALLE
                                                                                                                                                                                                                                                                                SFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLE
                                                                                                                                                                                                                                                                                                                                                                                                  MDLRYFPMDRQACTIEIE------SFGYTMKDIRYRWSDGDTSVRIAKEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                      MDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCL
                                                                                                                       ASPEVSIVKTVGSCQVCPAAVASQGQ
                                                                                                                                                                                           YAAVGYLGK -- RITMRKTRCQQLAKLAEQHRQ-
                                                                                                                                                                                                                           YAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGI
                                                                                                                                                                                                                                                                                                                                 PQFKVLGHVQKAKEVALTTGNYS--RLVC-EIRF--ARSMGYYLIQIYIPAGLIVVISWV
                                                                                                                                                                                                                                                                                                                                                   PQF----ILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRGYDRRVRPNYGGVPVEVGVTMQIISISTVSEVQMDFTSDFYFRQSWRDERLSFQKSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   537 AA;
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                                    Protein;
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                                    456 AA
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Pred. No. 4.6e-67;
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Best Local S
Matches 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel Drosophila glutamate gated chloride channel (GluCl) (AAW05246) is selectively opened by either avermectin or glutamate and represents a target of avermectin action in arthropods. Its amino acid sequence was deduced from a Drosophila head cDNA clone (AAT43596)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glutamate gated chloride channel; GluCl; ligand gated channel; avermectin binding protein; glutamate binding protein; antiparasitic; anthelmintic; helminthiasis; ectoparasticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid sequence was deduced from a Drosophila head cDNA clone (AAT43596 Recombinant GluCl, or host cells expressing it, can be used to screen for modulators of GluCl that can be used as ectoparasitic, anthelmintic, acaricide or insecticide agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding protein agents for the t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiparasitic;
acaricide; ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila glutamate-gated chloride channel
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding Drosophila avermectin and/or glutamate binding protein - useful for isolating cpds. used as antiparasitic agents for the treatment or prevention of helminthiasis in domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-506147/50.
N-PSDB; AAT43596.
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                257 TCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQS
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                                                                                                                                                                                                             FINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANE
                                                                                                                                                      KGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILC
                                                                                                                                                                                         FVRSIMTISDIKMEYSVQLTFREQWTDERLKFDDIQGRLKYLTLTEANRVWMPDLFFSNE
                                                                                                                                                                                                                                                            ILYFASLCSASLANNAKVNFREKEKKVLDQILG-AGKYDARIRPSGINGTDGPAIVRINL
                                                                                                                                                                                                                                                                                             VLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNI
                                                  -----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEY
                                                                                 SPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKF
                                                                                                                      KEGHFHNIIMPNVYIRIFPNGSVLYSIRISLTLACPMNLKLYPLDRQICSLRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 45-46; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cully DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster strain Oregon
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23..456
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= :: =
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                                                                                                                                                                                                                                                                                                                                              Score 730.5;
Pred. No. 4e
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Length 456
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                                                                                              Query Match
Best Local Similarity
Matches 160; Conser
                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                Sequence
                                                                                                                                                                     The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 22155; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
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                                                                                                                                                                                                        (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid detection reagent
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                     GYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPD-D
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SYDKRYRPNYGGPPVEVGYTMYVLSISSLSEVKMDFTLDFYFRQFWTDPRLAYRKRPGVE
                                                LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISATLDSFSV
                                                                     VPATLSFLLLWTLPGQVLLRVALAKEE-----VKSGTKGSQPMSPSDFLDKLMGRTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606
                                                                                             Score 729; DB
Pred. No. 8.8e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Myers
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                                                                                                          DB 22;
.8e-67;
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                                                                                                                                                                                  format
                                                                                                                                                                               part of the printed format directly from
                                                                                                                    Length 606;
                                                                                                Indels
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hybridization and to insecticides w

which

detect and genotype insects affect the GABA receptor. 1

Introducing

(1)

into

which may be resistant

YX X

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RESULT 15
AAY51077
ID AAY51
encoding mutant invertebrate gamma aminobutyric acid (GABA) receptors Expression of the GABA receptor is used for drug and pesticide screening and for identifying GABA antagonists or agonists. The methods allow large numbers of compounds potentially useful as drugs or pesticides to be screened and to find compounds which overcome existing or potential resistance mechanisms e.g. pesticides which are capable of blocking GABA-gated chloride channels resistant to cyclodienes. (I) may be used to detect mutants by the polymerase chain reaction (PCR) and/or the polymerase chain reaction (PCR) and or the polymerase chain reacti
                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel purified and isolated nucleic acids (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila simulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GABA receptor; fruitfly; invertek pesticide resistance; GABA-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D. simulans GABA receptor variant RldMD-RR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY51077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and isolated nucleic acid encoding a mutant invertebrate GABA useful for drug and pesticide screening assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVIISWVSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Column 53-56;
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BA-gated chloride channel; cyclodiene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beneficial insect may render the insect resistant to a pesticide and can be used in combination with pesticides in the field to reduce or eliminate the presence of harmful insects only. The insect GABA receptor shows critical pharmacological differences from the vertebrate receptor which may result in the development of insect-specific insecticides with greater safety for vertebrate exposure. This sequence represents a variant Drosophila simulans (fruitfly) GABA receptor RIdMD-RR described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                            438 GPGGP 442
                             413 QPPAP 417
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                                                                                                                                   296 DAAPARVGLGITTVLTMTTQSSGSRASLPKVSYYKAIDIWMAVCLLEVFAALLEYAAINF 355
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                                                                                                                                                                                                                                                        176 LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ 235
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                                                                                      356 VSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHC---LQARDGGPMEGSGIYSP 412
                                                                                                                                                                                                                                                                                                                                                                             46 LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 VPATLSFLLLWTLPGQVLLRVALAKEE-----VKSGTKGSQPMSPSDFLDKLMGRTS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 32.2%; Score 726; DB 21; Similarity 36.7%; Pred. No. 1.9e-66;
                                                          MAK-----RIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVGVGPG 437
                                                                                                                  LQYFPMDRQLCHIEIE------SFGYTMRDIRYFWRDGLSSVGMSSEVELPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 637;
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Search completed: June 25, 2003, 17:15:32 Job time : 64.6734 secs

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
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21682.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_Aa:*

1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
6: /cgn2_6/ptodata/1/pubpaa/U
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11: /cgn2_6/ptodata/1/pubpaa/U
13: /cgn2_6/ptodata/1/pubpaa/U
14: /cgn2_6/ptodata/1/pubpaa/U
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length: 2000000000
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2252
1 MTTLVPATLSFLLL
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
   :/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
:/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compu
                                                                                                                                                                                                                                                                                                                                                        Length DB
US-10-075-846-12
US-10-075-846-15
US-10-075-846-11
US-10-075-846-14
US-09-969-844-14
US-09-808-602-87
US-09-988-602-87
US-09-988-39
US-09-910-689-39
                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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1307.255 Million cell updates/sec
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           sequence 13, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 39, Appl
                                                                                                                                                                                                                                                                                                                                                      Description
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 592.5 | 594.5 | 594.5 | 602 | 603 | 607 | 608 | 608 | 615 | 615 | 615 | 615 | 615 | 615 | 615 | 615 | 615 | 615 | 615 | 618 | 619.5 | 620 | 620 | 632.5 | 632.5 | 632.5 |
| 26.3 | 26.4 | 26.4 | 26.7 | 26.8 | 27.0 | 27.0 | 27.0 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.3 | 27.4 | 27.5 | 27.5 | 27.5 | 28.1 | 28.1 | 28.1 |
| 466 | 468 | 468 | 345 | 392 | 420 | 467 | 467 | 535 | 485 | 464 | 464 | 464 | 464 | 464 | 464 | 464 | 464 | 464 | 465 | 554 | 465 | 465 | 423 | 422 | 397 |
| 9 | 10 | 9 | 9 | 9 | 9 | 10 | 9 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 9 | 9 | 9 | 9 | 9 | 9 | 10 | 9 | 10 | 10 | 10 |
| US-09-839-446-8 | US-09-898-570-6 | US-09-839-446-6 | US-09-765-069-10 | US-09-765-069-4 | US-09-765-069-8 | US-09-742-311-2 | US-09-765-069-2 | US-09-808-483-10 | -09-808-48 | US-09-898-570-38 | -898-57 | US-09-898-570-36 | US-09-898-570-35 | US-09-742-311-4 | US-09-839-446-38 | US-09-839-446-37 | | US-09-839-446-35 | US-09-818-657-4 | US-10-211-673-8 | US-09-893-321-2 | US-09-818-657-2 | US-09-808-483-8 | US-09-808-483-4 | US-09-808-483-6 |
| Sequence 8, Appli | • | Sequence 6, Appli | 10, | Sequence 4, Appli | Sequence 8, Appli | | Sequence 2, Appli | 10, | 12, | 38, | | Sequence 36, Appl | Sequence 35, Appl | Sequence 4, Appli | ` | • | ` | ა ა | Sequence 4, Appli | Sequence 8, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 8, Appli | Sequence 4, Appli | Sequence 6, Appli |

ALIGNMENTS

RESULT 1 US-10-075-846-4

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Sequence 4, Application US/10075846
Publication No. US20030032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOTIFIE OF INVENTION: IN THE GASTROINTESTINAL TRAFFILE REFERENCE: DO079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTMARE: Patentin version 3.0
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-075-846-4
                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 431; Conservative (
                                  181 MDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRD 240
                                                                                                               61
                                                                                                                                                                                                                 61 RIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLD 120
                                                                                                                                                                                                                                                                     EKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA 300
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Pred. No. 1.1e-206;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 431;
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A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI TRACT, HGRA4, and SPLICE VARIANT THER

Length

21;

Gaps

142

191 202

247

382

367

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREO
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 417
TYPE: PRT
ORGANISM: homo sapiens
US-10-075-846-2
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Best Local S
Matches 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                         421
        407
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                                                                                                                                         PSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFP 180
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                                        EGETTRKLYVD 431
                                                                                          KEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGIYSPQPPAPLLR 420
                                                                                                                                                                                                                              EKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPA
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        EGETTRKLYVD 417
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Pred. No. 3.4e-198;
0; Mismatches 1;
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publication No. US/20030032608A1
GENERAL INFORMATION:
APPLICANY: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A PITTLE OF INVENTION: IN THE GASTROINTESTINAL TRAFFILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
CURRENT FILING DATE: 2002-02-13
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US-10-075-846-13
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PRIOR APPLICATION NUMBER: US 60/269,535;
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
1.FM/GMT: 1
GENERAL INC. USACUSUOSAL
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNI
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THER
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 337
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Matches
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TYPE: PRT
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ORGANISM: Homo sapiens
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SRENESGYGMGHCLQVKDGTAVKATPANPLPQPP----KDGDAIKKKFVD 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPS
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PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 312
TYPE: PRT
ORGANISM: homo sapiens
US-10-075-846-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: UNSURE
; LOCATION: (322)..(322)
; OTHER INFORMATION: wherein "X"
US-10-075-846-12
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US-10-075-846-15
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL GLYCINE RECEPTOR ALPHA SUBUNIT E
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACT, HGRA4, and SPLICE VARIANT THEREOF
FILE REFERENCE: D0079 NP
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                                                                                                                                              PSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWN 103
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No. US20030032608A1
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Pred. No. 5.5e-152;
7; Mismatches 7;
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RESULT 7
US-10-075-846-10
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APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.0 SEQ ID NO 11
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Best Local
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----SFGYTMNDLIFEWQDEAP-VQVAEGLTLPQFILKEEKDLRYCTKHYNTGKFTCIEV
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Pred. No. 1.4e-144;
5; Mismatches 43;
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Sequence 10, Application US/10075846
Publication No. US/2003032608A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A I
TITLE OF INVENTION: IN THE GASTROINTESTINAL TRACE
FILE REFERENCE: D0079 NP
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/269,535
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 10
LENGTH: 449
TYPER: DBT
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US-10-075-846-14
US-10-075-846-14
; Sequence 14, Application US/10075846
; Publication No. US20030032608A1
                           ; TYPE: PRT ; ORGANISM: homo sapiens US-10-075-846-14
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
TITLE OF INVENTION: IN THE GASTROINTESTINAL
FILE REFERENCE: D0079 NP
CURRENT APPLICATION NUMBER: US/10/075,846
CURRENT FILING DATE: 2002-02-13
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LENGTH: 298
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.0
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Pred. No. 1.7e-142;
8; Mismatches 50;
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Publication No. US20020192776A1
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Best Local Similarity
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APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A33815-1 072667 0178
CURRENT APPLICATION NUMBER: US/09/969,844
CURRENT FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                           TTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP---NFKGPPVNVTCNIFINSFSSVTK
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REFSYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVLLGVTTLLTMATQSSGINASLPPV
                                                                                                                                                                                                        PNVYIRIFPNGNVLYSIRISLTLSCPMNLKLYPLDKQTCSLRM-----
                                                                                                                                                                                                                                                       DNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSV 207
                                                                                                                                                                                                                                                                                                             VTMEYSVQLTFREQWLDERLKFNNLGGRLKYLTLTEANRVWMPDLFFSNEKEGHFHNIIM 144
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                                                RQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKV 326
                                                                                                    GWTTDDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEYSCLKVDLLFK
                                                                                                                                                  GYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKFTCIEVKFHLE
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Pred. No. 6.7e-62;
3; Mismatches 111
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RESULT 11
US-09-800-198-74
Sequence 74, Application US/09800198
Publication No. US20030087816A1
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US-09-808-602-87
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PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 87
LENGTH: 533
TYPE: PRT
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       GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vernet,
APPLICANT: Fernanc
APPLICANT: Shimket
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PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/808,602
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MacDougall, John TITLE OF INVENTION: No. US20020155115Alel Proteins and Nuclec Acids Encoding Same FILE REFERENCE: 15966-697 CIP
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Herrman, John L
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Mezes, Peter S
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Pred. No. 1.5e-60;
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CURRENT APPLICATION NUMBER: US/10/239,420
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/US01/09956
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/193,935
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         RESULT 12
US-10-239-420-2
                                                                                                                                                                                                                                  Sequence 2, Application US/10239420 Publication No. US20030096984A1 GENERAL INFORMATION:
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LENGTH: 533
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Matches 146; Conserv
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CURRENT APPLICATION NUMBER: US/09/800,198.
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1.
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                                                                                                                                              TITLE OF INVENTION: DNA MOLECULES ENCODING LIGAND TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VAR FILE REFERENCE: 20629P
                                                                                                                                                                                                APPLICANT: Cully, Doris F. APPLICANT: Zheng, Yingcong
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APPLICANT:
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TYPE: PRT
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Mishra, Vishna
Mezes, Peter S
Rastelli, Luca
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; Pred. No. 1.5e-60;
80; Mismatches 122
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LENGTH: 397
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Best Local Similarity
INFORMATION
                                                                                                                                 APPLICATION NUMBER: PCT/GB95/02323 FILING DATE: 29-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Le Bourdelles, Beatrice
Whiting, Paul John
TITLE OF INVENTION: HUMAN ALPHA 4 RECEPTOR SUBUNIT
                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                         APPLICATION NUMBER: US/10/211,673 FILING DATE: 02-Aug-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTTLGVTTLLTISSKGSGIQSNLPPVSYVKAIDVWMGACTGFVFSALLEFTVVSCLAR 330
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ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E.
                              TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ fo
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rahway
                                                                                                   REGISTRATION NUMBER: 45,243
                                                TELEPHONE:
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Pred. No. 2.9e-60;
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                                                                                  T1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Lincoln Ave
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                                                                                                                                                      US-10-239-420-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-239-420-5
                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 422
                                                                          Matches
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10239420 Publication No. US20030096984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/239,420 CURRENT FILING DATE: ~2002-09-23 PRIOR APPLICATION NUMBER: PCT/US01/09956 PRIOR FILING DATE: 2001-03-28 PRIOR APPLICATION NUMBER: 60/193,935 PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cully, Doris F.
APPLICANT: .Zheng, Yingcong
TITLE OF INVENTION: DAN MOLECULES ENCODING LIGAND GATED IO
TITLE OF INVENTION: CHANNELS FROM DERMACENTOR VARIABILIS
FILE REFERENCE: 20629P
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                       ORGANISM: Dermacentor variabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 DLEFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 SRPRAEMDV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 YNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141;
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   53
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                                   48 LDKLMGRTSGYDARIRP-NFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 PGQVLLRVALAKEEVKSGTKGSQPMS-----PSDFLDKLMGRTSGYDARIRPNFKGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PARLLAPLLLLCAQQLRGTRAMNDIGDYYGSNLEISWLPNLDGLIAGYARNFRPGIGGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSAGQFPRLSLHFHLRRNRGVYIIQSYMPSVLLVAMSWVSFWISQAAVPARVSLGITTVL
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LDNILW---SYDRRITPGHHLNVPTVVKCEIYLRSFGAVNPATMDYDVDLYLRQTWTDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRQRLEEDI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKH 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTFIVNAKSAWFHDVTVENKLIRLQPDGVILYSIRITSTVÁCDMDLAKFPMDEQECMLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TMTTLMVSARSSLPRASAIKALDVYFWICYVFVFAALVEYAFAHF-NADYRKKQKAKVKV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-----SYGYSSEDIVYYWSESQEHIHGLDKLQLAQFTITSYRFTTELMNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                           Conservative
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                                                                                           29.1%;
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                                                                        75;
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                                                                        Score 655; DB y; _
Pred. No. 4.1e-54;
Pred. No. 4.1e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137;
                                                                                                               Length 422;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF BREAST CANCER
FILE REFERENCE: 20121.491C1
CURRENT APPLICATION NUMBER: US/09/510,662A
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 41
SOSTWARE: Patentin Ver. 2.0
SEQ ID NO 39
SEQ ID NO 39
TYPE: PRT
ORGANISM: Homo sapiens
US-09-510-662A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09510662A Patent No. US20020155125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Wang, Aljun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 LSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFA 345
:||||||:::|| ||:||:||:|| :|:|| ||:|||||:|||
273 VSWVSFWLDVDAIPARITLGVTTLLTISSESSDHQANLAPVSYVKALDVWMGTCTMFVFA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 QFILRDEKDLGCCTK-HYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWI 293
                                                                                                                                                                                                                                       175 DLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLP 234
                                                                                                                                                                                                                                                                                         333 AVLEFTFVSYLARR 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 TMYSGLKMAQFELQ-QISLTKCSGAFQIGEYSCLRAELNLKRSIGHHLVQSYLPSTLIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 QVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 LKLTESCHMINNERYPLDRQVCSIELASES------KTTKEVELQW-GNAEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 LTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAV 225
327 AHYSSLQQ----MAAKDRGTTKEVEEVSITNIINSSISSFK 363
                                                                                                                                            209 QYTI--ERYFTLVTRSQQETGNYTRLVLQFELRRNVLYFILETYVPSTFLVVLSWVSFWI 266
                                                                                                                                                                                                                   163 DLSKYPMDTQTCKLQLE------SWGYDGNDVEFTWLRGNDSVRGLEHLRLA 208
                                353 INFVSRQHKEFIRLRRRQRRQRLEE----DIIQESRFYFR 388
                                                                                                                                                                                                                                                                                                                                                                  45 TAGYNKFLRPNEGGEPVQIALTLDIASISSISESNMDYTATIYLRQRWMDQRLVFE--GN 102
                                                                                                                                                                                                                                                                                                                                                                                             55 TSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYRBYPD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Search completed: June 25, 2003, 17:18:50

Job time : 37.6756 secs

(OPPEU) NNAJ8 3DA9 ZIHT

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Result
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq length: 0
DB seq length; 2000000000
     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-075-846-4
2252
1 MTTLVPATLSFLLL
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   MTTLVPATLSFLLLWTLPGQ.....PQPPAPLLREGETTRKLYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/11/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/11/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/11/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/11/1aa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
     В
US-08-137-614A-24
US-09-130-339-2
US-08-435-933-6
PCT-US96-06035-6
US-09-02-361-6
US-09-02-361-6
US-09-02-361-5
US-09-02-361-5
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score 745; DBPred. No. 2.9eMismatches

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Length 617; Indels

34;

Gaps

63 IDSLL---KGYDIRLRPSFGGAPLEIGIEVILASFDSISEVDMDYTITMYLNQYWRDERL

| RESULT 1 US-08-137-614A-24 Sequence 24, Application US/08137614A Sequence 24, Application US/08137614A Patent No. 5487976 GENERAL INFORMATION: APPLICANT: Soderlund, David M. APPLICANT: Knipple, Douglas C. APPLICANT: Knipple, Douglas C. APPLICANT: Henderson, Joseph E. TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Rece NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/137,614A FILING DATE: 15-OCT-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: TILDHONE: (716)263-160 INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 617 amino acids TYPE: amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein | 28 673 29.9 487 1 US-08-249-112-4 29 673 29.9 487 5 PCT-US95-06556-4 30 670.5 29.8 510 1 US-08-249-112-3 31 670.5 29.8 510 5 PCT-US95-06556-3 32 663 29.4 506 4 US-09-627-650B-15 33 663 29.4 506 4 US-09-627-650B-14 35 657 29.2 487 4 US-09-627-650B-14 36 656 29.1 475 4 US-09-436-063C-14 37 656 29.1 475 4 US-09-436-063C-16 37 656 29.1 475 4 US-09-436-063C-16 38 652.5 29.0 440 1 US-08-459-100A-2 40 644.5 28.6 453 1 US-08-459-100A-2 41 628 27.9 686 2 US-08-768-301-4 42 619.5 27.5 554 4 US-08-469-100A-3 43 619.5 27.5 554 4 US-08-417-330A-12 45 610.5 27.1 492 1 US-08-417-330A-14 5 610.5 27.1 492 1 US-08-417-330A-14 |
|---|---|
| Receptor Subunit | Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 15, Appl Sequence 15, Appl Sequence 14, Appl Sequence 16, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 18, Appli Sequence 18, Appli Sequence 3, Appli Sequence 3, Appli Sequence 18, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Sequence 17, Appli |

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APPLICANT: Xiao-Zhou Michelle Wang
APPLICANT: Xavier Georges Sarda
APPLICANT: Michael David Tomalski
APPLICANT: Winchel David Tomalski
APPLICANT: Vincent Paul Mary Wingate
TITLE OF INVENTION: Heliothis Glutamate Receptor
FILE REFERENCE: A32815 072667.0118
CURRENT FAPLICATION NUMBER: US/09/592,891A
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 450
TYPE: PRT
TYPE: PRT
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Paress, Philip S.
APPLICANT: Liu, Ken K.
APPLICANT
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08435933 Patent No. 5693492
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APPLICANT: Cohen, Charles J.
APPLICANT: Brochu, Richard M.
APPLICANT: Brochu, Richard M.
TITLE OF INVENTION: DNA MOLECULES ENCODING CTENOCEPHALIDES
TITLE OF INVENTION: FELIS GLUTAMATE GATED CHLORIDE CHANNELS
FILE REFERENCE: 20029
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APPLICANT: Paress, Philip S.
APPLICANT: Warmke, Jeffrey W.
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                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
                                                    STREET:
                        STATE:
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                                            Rahway
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                                                                    126 East Lincoln Avenue
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Pred._No. 4.9e
60; Mismatches
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                                                                                                                     Sequence 6, Application PC/TUS9606035
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                       APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: CHANNELS
NUMBER OF SEQUENCES: 6
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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LENGTH: 456 amino acid
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              CORRESPONDENCE ADDRESS:
ADDRESSEE: Jody M. Glesser
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NAME: Wallen, III John W.
                                                                                                        APPLICANT:
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REFERENCE/DOCKET NUMBER: 19264
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54; Conservative
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126 East Lincoln Avenue -
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                                                                                                   Cully, Doris F.
Arena, Joseph P.
Paress, Philip S.
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Pred. No. 6.3e-69;
1; Mismatches 120;
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BOX 2000-0907
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RESULT 6
US-09-627-650B-19
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                   GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors
TITLE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
                                                                                                                                                         Sequence 19, Application US/09627650B Patent No. 6406872
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/627,650B
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Giesser, Jody M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                 Sequence 8, Applic Patent No. 6008046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/107,727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 1999-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE:
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OTHER INFORMATION:
OTHER INFORMATION:
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TYPE: PRT
SOFTWARE: PATENTIN RELATION DATA:
CURRENT APPLICATION NUMBER: US.
FILING DATE: 19930602
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                  APPLICANT: FFRENCH-CONSTANT, RICHARD APPLICANT: JACKSON, MEYER B.
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                     San Francisco
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220 Montgomery Stre
                                                                                                                                                    United States
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                                                    PatentIn Release #1.0,
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37.78;
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ER: 09/436,063
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                                                                                                                                                    of America
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Pred. No. 6.3e-69;
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Best Local S
Matches 156
                                                                                                                                                                 Sequence 6, Application US/09002361
Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blaik
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                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acid
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FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 COMPUTER
                                                                                                                     NUMBER OF SEQUENCES:
                                                           CITY:
                                                                        STREET:
                          COUNTRY:
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                                                          Lawrenceville
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READABLE FORM
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                                                                        E: Dechert Price 997 Lenox Drive,
                               USA
                                                                                                                                                                Halling,
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Building
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Pred. No. 3.
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US-09-002-361-3
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                                                                                                                                                          Sequence 3, Application US/09002361 Patent No. 6329516
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 153;
                                                                                    GENERAL INFORMATION:
APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
TITLE OF INVENTION: Channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 459 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wir CURRENT APPLICATION DATA:
                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   STREET:
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COMPUTER: I
                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 32.2%; Score 724.5; DB 4;
Similarity 37.8%; Pred. No. 2.7e-68;
53; Conservative 79; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
SEE: Dechert Price & Rhoads: 997 Lenox Drive, Building Lawrenceville
                                                                                                                                                                                                                                                                                               ------DGGPME------GSGIYSPQPPAPLLREGETTRKL 428
                                                                                                                                                                                                                                                                                                                                                                     INFVSR----QHKEFIRLRRRQRRQRLEEDI--IQESRFYFRGYGLGHCLQAR-----
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FastSEQ for Windows Version
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                                                                                   Sequence 5, Application US/09002361 Patent No. 6329516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
            GENERAL INFORMATION:
APPLICANT: Halling,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
NUMBER
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 PRLSYREYPD-DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS 163
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                                                                                                                                                                                            DGPPGSAEPIPPPRTSTLSRPPPP
                                                                                                                                                                                                                               DGGPMEGSGIYSP-----QPPAP 417
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SEQUENCES:
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              Channels
                                 Lepidopteran GABA-Gated Chloride
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Pred. No. 2.8e-68;
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   Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
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ADDRESSEE: Dechert Price & Rhoads
STREET: 97 Lenox Drive, Building 3, Suite
CITY: Lawrenceville
STATE: NJ
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
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   Application US/09002361
                                                                                                                                                            VGYMAKRIQMRKQRFVAIQKIASEKKIPVDCPPVGDPHTLSKMGTLGRCPPGRPSEVRFK
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                                                                                        VHDPKAHSKGGTLENTINGGRSGAEEENPGPPPHILHPGKDISKL 432
                                                                                                                         -----DGGPME-----GSGIYSPQPPAPLLREGETTRKL 428
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Pred. No. 3e-
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Best Local Similarity
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MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
TITLE OF INVENTION: Channels
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
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ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CON
OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 99/ LC...
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                  400
                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                          105 PRLSYREYPD-DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS 163
                                                     322 FVMVFASLLEYATVGYMAK-----RIQMRKQRFTAVQKMAAEKKMQI---
                                                                                  340 LLFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQAR
                                                                                                                         262
                                                                                                                                                          280
                                                                                                                                                                                             207
                                                                                                                                                                                                                               224 AVQVAEGLTLPQFILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP
                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                45 SDFLDKLMGRTSGYDARIRPNEKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQOWND 104
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DGGPMEGSGIYSP-----QPPAP
                                                                                                                                                         SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
                                                                                                                                                                                                                                                                  IRLTITASCPMDLQYFPMDRQLCNIEIE-----SFGYTMRDIRYKWNEGPN
                                                                                                                                                                                                                                                                                                     IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                                                                                                                                                                                                                                                                                                                                        PRLAYKKRTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRS
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                                                                                                                       SGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
                                                                                                                                                                                            SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVRSMGYYLIQIYIP
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FastSEQ for Windows Version
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.2%; Score 724.5; DB 4; 39.6%; Pred. No. 3.1e-68;
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Gaps

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DGPPGSAEPIPPPRTSTLSRPPPP 387

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 9732
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
TITLE OF INVENTION: LEPIDOPTERAN G
TITLE OF INVENTION: AND METHODS OF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 488 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
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                                                                                                                                                                                                                                                                                               LLFVFAALLEYAAINFVSRQHKEFIRLRRRQRR----QRLEED---------
                                                                                                                        SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
                                                                                                                                                                                           AVQVAEGLTLPQFILRDEKDLG----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP
                                                                                                                                                                                                                                 IRLTITASCPMDLQYFPMDRQLCNIEIE-----
                                                                                                                                                                                                                                                     IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                     FVMVFTSLLEYATVGYMAK-----
                                                                                                                                                          SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIP
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                                                                                         SGLIVIISWVSFWLNRNATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
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ER: 9732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 720; DB 1;
Pred. No. 9.1e-68;
                  -RIQMRKQRFTAVQKMQIDGPPGSAEPIPPPRTSTL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 488;
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                                                                                                                                                                                                                              --SFGYTMRDIRYKWNEGPN 206
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US-08-554-659-4
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Best Local S
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APPLICANT: Wingate, Vincent
APPLICANT: Wolff, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
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                                                                                                                                                     224 AVQVAEGLTLPQFILRDEKDLG-----CCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIP 279
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                                                                                                                                                                                                                                                                                             105 PRLSYREYPD-DSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYS
                340 LLFVFAALLEYAAINFVSRQHKEFIRLRRQRR----QRLEED--
                                                                                                                                                                                                                                                                                                                                                                                                       156;
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                                                                                                                                                                                                                                                                                                                                                      45 SDELDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWND 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11530-0299
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T: 400 Garden City Plaza
Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                    SGLIVIISWVSEWLNRNATPARVALGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTC
                                                                                     SLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVC
                                                                                                                        SVGVSSEVSLPQF-----KVLGHRQRAMEISLTTGNYSRLACEIQFVGSMGYYLIQIYIP
                                                                                                                                                                                                                              IRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAP
                                                                                                                                                                                                                                                                PRLAYKKSTGVETLSVGSEFIRNIWVPDTFFVNEKQSYFHIATTSNEFIRIHHSGSITRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 488 amino acids
amino acid
                                                                                                                                                                                             IRLTITASCPMDLQYFPMDRQLCNIEIE------SFGYTMRDIRYKWNEGPN
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                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (516) 742-4343
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339

261

378 321 223 160 163 100

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LEPIDOPTERAN GABA GATED CHLORIDE CHANNEL TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 SRPPPSRLSEVRFKVHDPKAYSKGGTLENTINGARGQP-----GPAPPA
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                       Score 720; DB 1;
Pred. No. 9.1e-68;
106;
                                           Length 488
Indels
74;
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Gaps
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376

US-08-072-064-1 RESULT 14

Patent No. 6008046 GENERAL INFORMATION:

Application US/08072064

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: TITLE OF INVENTION:

375

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CHROMOSOME/SEGMENT: III; polytene subregion MAP POSITION: approximately map unit 26
                                                                                                                                  100 SYDKRVRPNYGGPPVEVGVTMYVLSISSVSEVLMDFTLDFYFRQFWTDPRLAYRKRPGVE 159
                                                                                                                                                        57 GYDARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVELRQQWNDPRLSYREYPD-D 115
                                                                                                                                                                                                                                                5 VPATLSFLLLWTLPGQVLLRVALAKEE------VKSGTKGSQPMSPSDFLDKLMGRTS 56
    LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ 235
                                                          TLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGSITRSIRLTITASCPMN 219
                                                                                                                                                                                                              LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV 99
                                                                              SLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMD 175
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                                                                                                                                                                                                                                                                                        32.0%; Score 720; DB 3; I
36.5%; Pred. No. 1.4e-67;
tive 86; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite
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; Sequence 4, A
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Patent No. 6008046
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,83
                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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OPERATING SYSTEM:
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CITY: San
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                            57 GYDARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVELRQQWNDPRLSYREYPD-D 115
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                                                                      46 LPRT-PLLTIW-----LAINMALIAQETGHKRIHTVQAATGGGSMLGDVNISAILDSFSV 99
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                                                                                                                                                      Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      Score 720; DB 3;
Pred. No. 1.4e-67;
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US-08-072-064-1

Query Match Best Local S Matches 155

Local Similarity nes 155; Conserv

Conservative

TELEFAX: 415/3/
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID

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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPTELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410

OPHD-00574

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.

CARROLL, PETER G.

CLASSIFICATION: APPLICATION NUMBER: FILING DATE: 19930

19930602

US/08/072,064

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

COUNTRY:

STREET:

San Francisco

220 Montgomery Street,

PETER G. CARROLL

California

United States of America

ADDRESSEE:

MOLECULE TYPE: ORIGINAL SOURCE:

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POSITION IN GENOME

ORGANISM:

Drosophila melanogaster

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| complet me : 25. | 438 | 413 | 385 | 356 | 325 | 296 | 266 | 236 | 220 | 176 | 160 | 116 |
| Search completed: June 25, 2003, 17:18:06 Job time : 25.1409 secs | 438 GPGGP 442 | 413 QPPAP 417 | MAKRIQMRKQRFMAIQKIAEQKKQQLDGANQQQANPNPNANVGGP-GGVGVGPG 437 | VSROHKEFIRLRRRQRRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGIYSP 412 | NATPARVSLGVTTVLTMTTLMSSTNAALPKISYVKSIDVYLGTCFVMVFASLLEYATVGY 384 | 296 DAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINF 355 | 266 FRVLGHRQ-RATEINLTTGNYSRLACEIQFVRSMGYYLIQIYIPSGLIVVISWVSFWLNR 324 | FILRDEKDLGCCTR | 220 LQYFPMDRQLCHIEIESFGYTMRDIRYFWRDGLSSVGMSSEVELPQ 265 | LKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQ 235 | 160 TLSVGSEFIKNIWVPDTFFVNEKQSYFHIATTSNEFIRVHHSGSITRSIRLTITASCPMN 219 | 116 SLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMD 175 |

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Result
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| Qy Db | Db Qy Db | Qy Qy Db | Query Best L Matche Qy | 30 31 31 32 33 33 34 41 41 41 42 43 43 43 44 44 45 47 47 47 47 47 47 47 47 47 47 |
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| 325 KVSYVKAIDIWMAVCLLEVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRL | 205 LSVGYMKDLVFEWLEDAPAVQVAEGLTLPQFTLROEKDLGCCTKHYNTGKFTCIEVKF | 85 VTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPD : | Match 74.9%; Score 1687; DB 2; ocal Similarity 92.3%; pred. No. 3.7e-137; s 324; Conservative 7; Mismatches 6; 25 VALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRP | 692 30.7 473 2 S53532 690 30.6 473 2 S04466 687.5 30.5 476 2 S11440 687.5 30.5 437 2 S34469 673.5 29.8 461 2 S50864 668.5 29.5 449 2 A34625 664.5 29.0 449 2 A36303 653.5 29.0 449 2 T20754 648.5 28.8 449 2 T20754 648.5 28.6 45 2 T207614 634.5 28.2 453 2 S11087 634.5 28.2 453 2 S11087 634.5 28.2 474 2 S13086 631.5 28.0 473 2 A38627 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| RLRRRORRORL 375 RLRRRORRORM 337 | GCCTKHYNTCKETCIEVKEH 264 | IWKPDLFFANEKGANFHE 1 | Length 337; Indels 14; Gaps 1; NFKGPPVNVTCNIFINSFSS 84 | gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric avermectin-sensiti gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric hypothetical prote GABAA receptor del gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric gamma-aminobutyric amma-aminobutyric gamma-aminobutyric |

RESULT 2 \$12381 glycine receptor alpha-2 chain - human

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C; Specie
C; Date:
                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30
C;Accession: S14816; S15776; JN0112
R;Akagi, H; Hiral, K; Hishinuma, F.
FEBS Lett 281, 160-166, 1991
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S14816
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 A; Molecule type: mRNA
A; Residues: 1-452 <KUI
A; Cross-references: GI
                                                                  A;Title: Alternative splicing A;Reference number: S15776; MI A;Accession: S15776
                                                                                                                  R; Kuhse, J.; Kuryatov, A.; Maulet, FEBS Lett. 283, 73-77, 1991
                                                                                                                                                                                                    A;Title: Cloning of a glycin
A;Reference number: S14816;
A;Accession: S14816
                                                                                                                                                                                                                                                                                                                                      glycine receptor alpha-2 chain variant A precursor N;Alternate names: neonatal glycine receptor
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A; Residues: 1-452 <GRE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Grenningloh, G.; Schmingloh, J. 9, 771-776, 1990
                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-452 < AKA>
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                                                                                                                                A;Cross-references: EMBL:X57281; NID:g56743; PIDN:CAA40549.1; PIR:Kuhse, J.; Kuryatov, A.; Maulet, Y.; Malosio, M.L.; Schmieden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Homo sapiens (man)
Date: 21-Nov-1993 #sequence
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                 1-452 <KUH>
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   GB:X61159;
                                                                                                                                                                                                                    glycine receptor subtype expressed 14816; MUID:91200276; PMID:1707830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.78;
                                                  conceptual translation
                                                                                  MUID:91243883;
 NID:g288344;
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Pred. No. 1.3e
29; Mismatches
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                                                                               PMID:1645300
 PIDN: CAA43471.1;
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PID:g288345
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A; Molecule type: mRNA
A; Residues: 1-193, 'E', '195-452 <KU2>
A; Residues: 1-193, 'E', '195-452 <KU2>
C; Comment: Glycine reduces neuronal firing by activating this inhi
C; Superfamily: acetylcholine receptor
C; Superfamily: acetylcholine receptor
C; Keywords: glycoprotein; ion channel; neurotransmitter receptor;
F; 1-27/Domain: signal sequence #status predicted <SIG>
F; 28-452/Product: glycine receptor alpha-2 chain #status predicted
F; 253-280/Domain: transmembrane #status predicted <TM1>
F; 287-304/Domain: transmembrane #status predicted <TM2>
F; 287-304/Domain: transmembrane #status predicted <TM2>
A; Molecule type: mRNA
A; Residues: 1-452 <KUPA
C; Superfamily: acetylcholine receptor
C; Keywords: 9lycoprotein; membrane protein
F; 1-27/Domain: signal sequence #status predicted
F; 28-452/Product: 9lycine receptor alpha-2 chain
                                                                                                                                                                                                              R;Kuhse, J.
FEBS Lett.
                                                                                                                                                                                                                                                     glycine receptor alpha-2 chain precursor C; Species: Rattus norvegicus (Norway rat) C;Date: 19-Mar-1997 #sequence_revision 25 C;Accession: S18836
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A;Accession: JN0112
                                                                                                                             A; Status: preliminary
                                                                                                                                                 A;Title: Alternative splicing A;Reference number: S15776; Mt A;Accession: S18836
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F;72,103/Binding site: carbohydrate (Asn) (covalent) #status
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Neuron 5, 867-873, 1990
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t. 283, 73-77,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                -KDADAIKKKFVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINEVSRQ 359
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                                                                                                                                                                                                                                                                                                                    chain precursor variant B
                                                                                                                                                                                                                                   Maulet, Y.; Malosio, M.L.; Schmieden,
                                                                                                                                                                                                                                                                                                                                                                                                                                413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431
                                                                                                                                                                       ng generates two isoforms of MUID:91243883; PMID:1645300
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                          <SIG>
      variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                             #text_change
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        predicted
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                                                                                                                                                                                                                                   Betz,
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#status

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RESULT 5

849970

91ycine receptor alpha-2 chain - mouse
91ycine receptor alpha-2 chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Mar-1999
C:Accession: 849970; S15802
                                                                                                                                                                                                 A;Title: Alternative splicing generates two isoforms of the alpha-2 subunit of the A;Reference number: S15776; MUID:91243883; PMID:1645300 A;Accession: S15802
                                                                                                                                                                                                                                                                                                                                    R:Matzenbach, B.; Maulet, Y.; Sefton, L.; Courtier, B.; Avner, P.; Guenet, J. Biol. Chem. 269, 2607-2612, 1994
A;Title: Structural analysis of mouse glycine receptor alpha subunit genes. A;Reference number: A49970; MUID:94132024; PMID:7507926
A;Accession: B49970
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A; Residues: 67-89
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                                                                                                                                                                                        A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                     FEBS
                                                                                                                                                                                                                                                               A;Cross-references: GB:X75841
R;Kuhse, J.; Kuryatov, A.; Ma
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-451 <MAT>
                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;103/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                  ;Superfamily: acetylcholine receptor; transmembrane protein
                                                           Query Match
Best Local
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Lett. 283, 73-77, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                          Match 73.6%; Score 1656.5; DB 2; Local Similarity 75.1%; Pred. No. 2.2e-134; es 325; Conservative 33; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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MTTLVPATLSFLLLWTLPGQVLLRVALAKE-EVKSGTKGSQPMSPSDFLDKLMGRTSGYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGIYS-PQPPAPL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LREGETTRKLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKEFLRLRRQKRQNKEEDVTRESRFNFSGYGMGHCLQVKDGTAVKATPANPLPQPP---
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                                                                                                                                                                            mRNA
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75.1%;
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Pred. No. 1.3e-135;
33; Mismatches 49;
                                                                                                                                                                                                                                                              Y.; Malosio, M.L.; Schmieden, V.; Betz,
                                                                       DB 2;
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A23682

A23682

glycine receptor alpha-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change
C;Accession: A23682
R;Kuhse, J. Schmieden, V.; Betz, H.
J. Biol. Chem. 265, 22317-22320, 1990
A;Title: Identification and functional expression of a novel lig
A;Reference number: A23682; MUID:91093073; PMID:2176214
A;Accession: A23682
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-464 <KUH>
A; Cross-references: GB:M55250; GB:M38385;
C; Superfamily: acetylcholine receptor
C; Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                              | LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHYNTGKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITT
                            KHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITT
                                                                    QLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCT
                                                                                                                                                                                    ARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINFVSRQ 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PMDVQTCTMQLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDL 119
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                                                                                                                                                                                                                   PPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HKEFIRLRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDGGPMEGSGIYS-PQPPAPL 418
                                                                                                                                                                                                                                                  LSGFYFWE----AALLLSLVATKETNSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKG
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                                                                                                                                                                                                                                                                                                                    70.78;
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                                                                                                                                                                                                                                                                                                                      Pred. No. 8e-129;
                                                                                                                                                                                                                                                                                                                                    Score 1592;
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            NID:g204882; PIDN:AAA63492.1;
                                                                                                                                                                                                                                                                                                                                  DB 2;
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R:Matzenbach, B.; Maulet, Y.; Sefton, L.; Courtier, B.; Avner, P.; Guenet, J.L.; Betz, I. Biol. Chem. 269, 2607-2612, 1994
A;Title: Structural analysis of mouse glycine receptor alpha subunit genes. Identificati A;Reference number: A49970; MUID:94132024; PMID:7507926
A;Accession: C49970
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C49970
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FEBS Lett. 350, 71-76, 1994
A;Title: Point mutation of 91ycine receptor alpha-1 subunit
A;Reference number: S48662; MUID:94341377; PMID:8062927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycine receptor alpha-1 chain - mouse c;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 17-Mar-1999 C;Accession: C49970; S48662
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A; Residues: 62-84 <SAU>
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A; Residues: 1-451 <MAT>
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                                                            RRQRRQRLEEDIIQESRFYFRGYGLG-HCLQARDGGPMEGSGIYSP--QPPAPLLREGET
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C:Superfamily: acetylcholine receptor
C:Keywords: transmembrane protein
A; Molecule type: mRNA
A; Residues: 1-457 < MALJ.
A; Cross-references: EMBL: X55246; NID: g56468; PIDN: CAA38987.1;
A; Cross-references: EMBL: X55246; NID: g56468; PIDN: CAA38987.1;
A; Malosio, M.L.; Grenningloh, G.; Kuhse, J.; Schmieden, V.; ScJ. Biol. Chem. 266, 2048-2053, 1991
                                                                                                                                                                                                                 glycine receptor alpha-1 chain - rat
C;SpecLes: Rattus norvegicus (Norway rat)
C;Date: 20-reb-1995 #sequence_revision 20-Feb-1995
C;Accession: S20662; A38597; A27141
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A;Accession: S12382
                                                                                              A; Status: preliminary
                                                                                                                  A; Reference number: A; Accession: S20662
                                                                                                                                                          A; Description:
                                                                                                                                                                        R; Malosio, M.; Kuhse, J.; Betz, H. submitted to the EMBL Data Library, December
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A; Residues: 1-449 < GRE>
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                                                                                                                                      S20662
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38; Mismatches
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                    Schmitt,
                                        PID:g56469
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glycine receptor beta chain - mouse () Species: Mus musculus (house mouse) () Species: Mus musculus (house mouse) () C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999 () Accession: $46459; 148371; 148372 R;Kingsmore, S.F.; Giros, B.; Suh, D.; Bieniarz, M.; Caron, M.G.; Seldin, M. Nature Genet. 7, 136-141, 1994 A;Title: Glycine receptor beta-subunit gene mutation in spastic mouse associ A;Reference number: $46459; MUID:95004576; PMID:7920630 A;Accession: $46459.
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A; Residues: 23-353,362-457 <GRE>
C; Superfamily: acetylcholine receptor
C; Keywords: alternative splicing
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A;Title: The strychnine-binding subunit of A:Reference number: A27141; MUID:87258250; A:Accession: A27141
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A;Residues: 316-378 <MA2>
A;Cross-references: GB:M63915; NID:g204426; PIDN:AAA63489.1;
A;Croningloh, G.; Rienitz, A.; Schmitt, B.; Methfessel, C.;
A;Molecule type: mRNA
A;Residues: 1-496 <KINN
A;Cross-references: EMBL:U09399; NID:g508234; PIDN:AAA61874.1; PID:g508235
A;Cross-references: EMBL:U09399; NID:g508234; PIDN:AAA61874.1; PID:g508235
R;Mulhardt, C.; Fischer, M.; Gass, P.; Simon-Chazottes, D.; Guenet, J.L.; Fineuron 13, 1003-1015, 1994
A;Title: The spastic mouse: aberrant splicing of glycine receptor beta subla;Reference number: I48371; MUID:95033198; PMID:7946325
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFK
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                                                                                                                                                                                                                                                                                                                                                                                                   417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SFGYTMNDLIFEWQEQG-AVQVADGLTLPQFILKEEKDLRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1568.5;
Pred. No. 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the glycine receptor shows PMID: 3037383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; DB 2;
0.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Zensen, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                         mouse associated
                       beta subunit mRNA
                                                                                                                                                                                                                              Seldin, M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
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                                                          Kuhse,
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 103-108;124-136;213-234 <GR2>
A; Experimental source: spinal cord, brain
C; Comment: The glycine receptor is a ligand-gated chloride channel in po
C; Comment: The glycine receptor contains two membrane-spanning subunits
C; Superfamily: acetylcholine receptor
C; Keywords: glycoprotein; phosphoprotein; transmembrane protein
F; 1-22/Domain: signal sequence *status predicted <SIG>
F; 23-496/Product: glycine receptor beta chain *status predicted <GRB>
F; 270-286/Domain: transmembrane *status predicted <TM1>
F; 289-316/Domain: transmembrane *status predicted <TM2>
                                                                                                                                                                                                                                                                                           A;Title: Cloning and expression of the 58 kd beta subunit of the inhibitory glycine A;Reference number: JH0165; MUID:90297968; PMID:2163264
A;Accession: JH0165
A;Molecule type: mRNA
A;Residues: 1-496 <GRE>
A;Accession: PS0296
A;Accession: PS0296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
JH0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 100-250 <RE2>
A;Cross-references: EMBL:X81201; NID:g557656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Grenningloh, G.; Pribilla,
Neuron 4, 963-970, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
C:Accession: JH0165; PS0296
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A; Introns: 176/2; 204/1
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A; Residues: 13-364, 'A', 366-496 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine receptor beta chain precursor - rat N; Alternate names: glycine receptor 58K chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AALLEYAAINFVSROHKEFIRLRRRORR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I.; Prior, P.; Multhaup, G.;
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Pred. No. 7.8e-67;
1; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beyreuther, K.; Taleb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PMSPSDFLDK
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                                                                                                                                                                      postsynaptic me
ts of 48kd, alph
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F;478-495/Domain: transmembrane #status predicted <TM4>
F;478-495/Domain: transmembrane #status predicted <TM4>
F;478-495/Domain: transmembrane #status predicted F;543,242-255/Disulfide bonds: #status predicted F;183-197,243-255/Disulfide bonds: #status predicted F;385,410/Binding site: phosphate (Thr) (covalent) #status predicted F;435/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:5875373;
A; Map position: 4q32-4q32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: G09080 A; Accession: G02031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: G02031
R; Handford, C.A.; S
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A; Residues: 1-497 <HAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                              Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                           Gene: GDB:GLRB
                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
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187; Conser
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                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
      --SYREYPODSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIR
                                              RLL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKL
                                                                                     KLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL--
                                                                                                                           TTAFLILISL----WVEEAYSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPANSTSNILN
                                                                                                                                                                    TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASLVEYAVVQVMLNNPKRVEAEKARIAKAEQ 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALLEYAAI ---- NFVSRQHKEFIRLRRRQR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-EKIALPOFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITLSCPLDLTLFPMDTQRCKMQLE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSFFILMSL----LFEDACSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPPNSTSNILNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ------
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schofield, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              translated
                                                                                                                                                                                                                             38.0%;
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47.8%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                    OMIM: 138492
                                                                                                                                                                                                                                                                                                                                                                                              NID: g992686; PIDN: AAB37750.1;
                                                                                                                                                                                                                                Score 855.5; DB 1
Pred. No. 1.7e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       August
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-Jun-1997 #text_change
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.ches 88;
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                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                            99;
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                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                            5
3
                                                                                                                                                                    -SPSDFLD
                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                Вb
                                                                                                                                                                                                                                                                ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein F;1-23/Domain: signal sequence #status predicted <SIG> F;24-499/Product: gamma-aminobutyric acid/benzodiazepine receptor A beta chain #statu F;24-499/Product: gamma-aminobutyric acid/benzodiazepine receptor A beta chain #status predi
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A; Residues: 201-231, 'L', 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Soc. Trans. 18, 438
A; Title: Cloning of genomic
A; Reference number: A60170;
A; Accession: A60170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X58638; NID:g9626
A;Note: the translated sequence in GanBank entry
R;Harvey, R.J.; Vreugdenhil, E.; Barnard, E.A.; [
Biochem. Soc. Trans. 18, 438-439, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-499 < HAR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown; not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Harvey, R.J.; Vreugdenhil, E.; Zaman, S.H.; Bhandal, N.S.; Usherwood, EMBO J. 10, 3239-3245, 1991
A; Title: Sequence of a functional invertebrate GABA(A) receptor subunit A; Raference number: S17785, MUID:92007774; PMID:1655414
A; Accession: S17785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Aug-1999
C;Accession: S17785; A60170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma-aminobutyric acid/benzodiazepine receptor A beta chain precursor - N; Alternate names: GABA(A) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                            48 LDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL
                                                                                                                                                                                                                                                                                                            37
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YIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTWTTQSSGSRASLPKVSYVKAIDIWM
                                                                                                                                                                                                                                                                      SYREYPDDSLDLDP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDER--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMR 176
                                                                YWLNDRGAVTGVEDVSLPQFSITNYATIN-KIEELSTGDYQRLSLIFQLQRNIGYFIFQT
                                                                                                                                                                                                                             QF--IFNESLDLGENRSVTTMTLTGAFAEKIWVPDTFLANDKNSFLHDITEKNKMVRLYG
                                                                                                                                                                                                                                                                                                            IDSLL---KGYDIRLRPSFGGAPLEIGIEVILASFDSISEVDMDYTITMYLNQYWRDERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAV 225
                                                                                                      EWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQM
                                                                                                                                                 NGSLVYGMRFTTTLACMMDLHNYPLDHQECTVEIE
                                                                                                                                                                                   NGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVF 216
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and cDNA sequences encoding an MUID:90323312; PMID:2164988
                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                       Score 742; DB 2; Pred. No. 9.6e-56; Smatches 90;
                                                                                                                                                                                                                                                                    SMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFK 156
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gamma-aminobutyric acid receptor A beta-4' chain precursor - chicken N;Contains: gamma-aminobutyric acid receptor A beta-4 chain, long splice for C;Species: Gallus gallus (chicken) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999 C;Accession: JH0359; JH0360; B61282; A61282; S29694; S29696; S29695 R;Bateson, A.N.; Lasham, A.; Darlison, M.G.
J. Neurochem. 56, 1437-1440, 1991
                                                                                                                                                                                                                                                                                                                                                       C;Keywords: alternative splicing; glycoprotein; neurotransmitter receptor; phosphoprotein; r:1-25/Domain: signal sequence #status predicted <SIG>
F;26-488/Product: gamma-aminobutyric acid A receptor beta-4' chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: gamma-aminobutyric acid A receptor beta-4 chain #status predicted <WF;26-360,365-488/Product: g
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A;Residues: 28-360,365-405 <BA4>
A;Cross-references: EMBL:X56648
C;Comment: The gamma-aminobutyric acid A receptor is the major inhibitory neurotransmit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 357-360,365-366 <LA2>
R; Bateson, A.N.; Lasham, A.; Darlison, M.G.
submitted to the EMBL Data Library, November 1990
A; Description: Gamma-aminobutyric acid-A receptor heterogeneity is increased
                                                                                                                                                                           F:304-326/Domain: transmembrane #status predicted <TM3>
F:466-487/Domain: transmembrane #status predicted <TM4>
F:32.104,173,195/Binding site: carbohydrate (Asn) (coval)
F:32.104,173,195/Binding site: predicted
                                                                                                                                                                                                                                                                                                      F;245-266/Domain: transmembrane #status predicted <TM1>F;271-292/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X56647; NID:g62916; A;Accession: S29695
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A; Residues: 1-405 <BA3>
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A; Accession: S29694
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A; Residues: 357-366 <LAS>
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Biochem. Soc. Trans. 19, 9S, 1991
A;Title: Alternative splicing increases GABA-A receptor heterogeneity.
A;Reference number: A61282; MUID:91244095; PMID:1645322
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A;Experimental source: brain
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A; Residues: 1-488 <BAT>
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A;Residues: 364-488 <BAW>
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                                                                                                                                                      448/Binding site:
                                                                   Local Similarity
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                                       Conservative
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                                                             32.2%;
                                                                                                                                                      (Ser)
                                       79;
                                                          Score 726;
Pred. No. 2.
                                                                                                                                                   (covalent) #status predicted
                                       Mismatches
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                                                             DB 2;
.2e-54;
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                                                                                        Length 488;
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                                 52;
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
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A; Residues: 1-533 <THO>
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Search completed: June 25, 2003, 17:17:34 Job time: 29.9262 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: June 25, 2003, 17:12:59; Search time 17.3557 Seconds (without alignments) 1029.995 Million cell updates/sec

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

US-10-075-846-4
2252
1 MTTLVPATLSFLLLWTLPGQ......PQPPAPLLREGETTRKLYVD 431

Scoring table:

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 26 27 28 30 31 33 | 15 16 17 19 20 21 22 23 24 | 6 7 8 10 11 12 13 | Result No. 1 2 3 |
|---|---|--|---|
| 687.5 676.5 664.5 663.5 653.5 644.5 | 726 720 715 712 712 712 712 695 695 694 694 691 691 | 1580.5 1580 1573 1569.5 1568.5 871 863.5 855.5 | Score 1682.5 1678 1670 1602.5 1592 |
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EMBL; X75853; CAA53468.1;
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InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRPAMS; TIGR00860; LIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPH MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAI
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sen the Swiss Institute of Bioinformatics and the Ex
European Bioinformatics Institute. There are no restr
                                                         PS00236; NEUROTR_ION_CHANNEL; Postsynaptic membrane; Ionic
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P22771; Q91W28;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-2* chain precursor (Neonatal isoform)
                                                                                        Kuhse J., Schmieden V., Betz H
"A single amino acid exchange
glycine receptor subunit.";
Neuron 5:867-873(1990).
                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
 MEDLINE-91243883;
                                                   Akagi H., Hirai K., Hishinuma F.;
                                                           MEDLINE=91200276;
                                                                  SEQUENCE FROM N.A. STRAIN-Wistar; TIS
                                                                                                                    MEDLINE-91097798;
                                                                                                                                                  NCBI_TaxID-10116;
                                                                                                                                                                         Rattus norvegicus
               SEQUENCE FROM N.A.
                                                                                                                                                                                       (Glycine receptor
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                             loning of a glycine receptor subtype expressed inal cord during a specific period of neuronal BS Lett. 281:160-166(1991).
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                                                          TISSUE-Spinal cord;
76; PubMed-1707830;
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                                                                                                                     PubMed=2176511;
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 PubMed-1645300;
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EXTRACELLULAR (PROBABLE).
POTENTIAL.
POTENTIAL.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1678; DB 1;
Pred. No. 1.3e-135;
Pred. No. 1.3e-135;
                                                                                                       alters
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Sciurognathi; Muridae
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                                                                                                                                    OF.
                                                                                                       the
                                                                                                                                    GLU-194
                                                                                                      pharmacology of
                                                                                                                                                          Muridae;
                                    in rat brain and development.";
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Murinae; Rat
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Betz H.;
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                                                                                                                                                                                                    X57281; CAA40549.1; -. X61159; CAA43471.1; -.
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-! ALFERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-2* (SHOWN HERE) AND ALPHA-2B ARE PRODUCED BY ALTERNATIVE SPLICING.
2B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-! TISSUE SPECIFICITY: THE GLYCINE RECEPTOR IS ABUNDANT IN THE SPINAL CORD AND BRAINSTEM OF VERTEBRATES.
-! DEVELOPMENTAL STAGE: THE ALPHA-2* SUBUNIT ISOFORM IS PRESENT IN NEONATAL RATS. ISOFORMS ALPHA-2B AND ALPHA-2B ARE PRESENT IN THE PRE- AND NEONATAL BRAIN. AT LATER POSTNATAL STAGES, ALPHA-2A LEVELS GREATLY DECREASE WHILE ALPHA-2B IS BARELY DETECTABLE.
-! MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNIME.
-! MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNIME.
-! MISCELLANEOUS: IDENTICAL TO THE HUMAN ALPHA-2 SUBUNIT, EXCEPT FOR SUBSTITUTIONS AT POSITIONS 18, 24, 37, 194 AND 404. SUBSTITUTION AT POSITIONS AT POSITIONS 18, 24, 37, 194 AND 404. SUBSTITUTION BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
-! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Alternative splicing generates two of the inhibitory glycine receptor FEBS Lett. 283:73-77(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beato M., Groot-Kormelink P.J., Colquhoun D., Sivilotti L.G.;
"Concentration dependence of single carriers through rat
recombinant alpha 1 glycine receptors.";
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
i- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER GATED ION
CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (51 SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERA MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS RECEPTOR CORE.
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PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Pfam; PF02931; Neur_chan_LBD; 1
Pfam; PF02932; Neur_chan_memb; InterPro; IPR000188; GABAA_receptor. InterPro; IPR001175; Neur_channel. family; BY SIMILARITY.
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N-LINKED (GLCN
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.) (POTENTIAL) AND STRYCHNINE

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RA Muelhardt C., Becker C.-M.;
RT Muelhardt C., Becker C.-M.;
RT Albert R.G., Lichter P., Kioschis P., Poustka A.,
RT Albert C., Becker C.-M.;
RT Chromosomal localization, and functional characterization of
Chromosomal localization, and functional characterization of
RT chromosomal localization, and functional characterization of
RT chromosomal localization, and functional characterization of
RT chromosomal localization, and functional characterization of
CC CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE
CC CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE
CC CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
CC CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
CC NEURONAL FIRING).
CC -1- SUBUNIT: PENTAMER COMPOSED OF LIGAND BINDING ALPHA (48 kDa) AND
STRUCTURAL BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (93
CC NDB) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE
CC CYTOPLASMIC DOMAINS OF THE RECEPTOR CORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                      075311; 075816;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Clycine receptor alpha-3 chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                   GRA3_HUMAN
                                                                                                                                                                                                        TISSUE=Fetal brain;
MEDLINE=98344067; PubMed=9677400;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              sapiens (Human)
ryota; Metazoa; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARVALGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAVNFVSRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWAVCLLFVFAALLEYAAINFVSRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARIRPNFKGPPVNVTCNIFINSFGSVTETTMDYRVNIFLRQQWNDSRLAYSEYPDDSLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARIRPNEKGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVNILTALFAFFL-----GTNHFREAFCKDHDSRSGKHPSQTLSPSDFLDKLMGRTSGYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KDADAIKKKFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt HKEFLRLRRRQKRQNKEEDVTRESRFNFSGYGMGHCLQVKDGTAVKATPANPLPQPP----} \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452
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                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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194
                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52053
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E->G: INCRE
STRYCHNINE.
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                         update)
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.3e-135;
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Best Local S
Matches 312
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EMBL; AF017718; AAC39919.1

EMBL; AF017719; AAC39919.1

EMBL; AF017720; AAC39919.1

EMBL; AF017721; AAC39919.1

EMBL; AF017721; AAC39919.1

EMBL; AF017723; AAC39919.1

EMBL; AF017723; AAC39917.1;
                                                                                                                                                                                                                                                                                            DISULFID DISULFID
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF017724; AAC39919.1;
EMBL; AF017715; AAC39919.1;
EMBL; AF017716; AAC39919.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERVOUS SYSTEM.

DOMAIN: THE N-TERMINAL DOMAIN CARRIES STRUCTURAL DETERMINANTS ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. TM2 IS THOUGHT TE ESSENTIAL FOR AGONIST AND ANTAGONIST BINDING. THE CYTOPLASMIC FORM THE INNERT WALL OF THE CHLORIDE CHANNEL THE CYTOPLASMIC IS AN IMPORTANT DETERMINANT OF CHANNEL INACTIVATION KINETICS.

MISCELLAMBOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA3L (SHOWN HERE)
ALPHA3K; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600421
                             142
141
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                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00236; NEUROTR_ION_CHANNEL;
                         FHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLP
                                                                       FSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN
                                                                                                                                 LLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
FHEVTTONKLLRIFKNGNVLYSIRLTLTLSCPMDLKNFPMDVQTCIMQLE---
                                                        FGSTAETTMDYRVN1FLRQKWNDPRLAYSEYPDDSLDLDPSMLDSTWKPDLFFANEKGAN
                                                                                                                  LLLSLVATKETDSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR00860;
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                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene
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73.8%;
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                                                                                                                                                                                                                                  BY SIMILARITY:
BY SIMILARITY:
N-LINKED (GLCNAC. . .
MISSING (IN ISOFORM A
MISSING (IN REF. 1; A
MISSING (IN REF. 1; A
                                                                                                                                                                                        Score 1602.5; DB 1; Pred. No. 5.5e-129;
                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                GLYCINE RECEPTOR
                                                                                                                                                                                                                                                                                                                          PROBABLE
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                                                                                                                                                                           43;
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                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                 . .) (POTENTIAL).
M ALPHA3K).
; AAC39917).
                                                                                                                                                                           Indels
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P24524;
                                                                                                                                                                                                   between
the Euro
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01-MAR-1992 (Rel. 21, Last sent
15-JUN-2002 (Rel. 41, Last anno
Glycine receptor alpha-3 chain
                                               PIR: A23682: A23682.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR0001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFINTS; PR002522; NRIONCHANNEL.
                                                                                                                                                   modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                         Kuhse J., Schmieden V., Betz H.;
"Identification and functional expression of a subunit of the inhibitory glycine receptor.";
J. Biol. Chem. 265:22317-22320(1990).
            PRINTS; FUNCTION TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
PS00236; NEUROTR_ION_CHANNEL;
PS00236; NEUROTR_ION_CHANNEL;
                                                                                                               EMBL; M55250;
PIR; A23682; /
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91093073; PubMed=2176214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL
                                                                                                                                                                                                                                                                                                   CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF MEURONAL FIRING).

SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL SUBUNITS. A THIRD TYPE OF SUBUNITH THE CYTOPLASMIC DOMAINS OF THE MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF TH
                                                                                                                                                                                                                                                                                                                                                               3101. Chem. 265:22317-22320(1990).
FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE C
                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                         RECEPTOR CORE
                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the ENEUROPEAN BIOINFORMATICS Institute. There are no rest
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                                                                                                                            AAA63492.1; -.
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   Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                    ormatics Institute. There are no restrictions institutions as long as its content is in
   family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464
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               channel;
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               Glycoprotein;
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; Murinae; Rat
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MBL outstation -
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                                                                                                                                                                            commercia.
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GRA1_HUMAN
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Best Local
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TRANSMEM
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DISULFID
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CHAIN
DOMAIN
TRANSMEM
TRANSMEM
SEQUENCE FROM N.A.

MEDLINE-90183975; PubMed-2155780;

Grenningloh G., Schmieden V., Schofield P.R., Seeburg P.H.,

Siddique T., Mohandas T.K., Becker C.-M., Betz H.;

*Alpha subunit variants of the human glycine receptor: primary

*structures, functional expression and chromosomal localization

corresponding genes.*;

EMBO J. 9:771-776(1990).
                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Glycine receptor alpha-1 chain precursor (G
                                                                                                                                                                                                                                      GRA1_HUMAN
P23415;
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SEQUENCE
                                                                                                                                                               GLRA1
                                                                                                                           Eukaryota;
Mammalia; E
                                                                                                                                                   Homo
                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                       RQRRQ----RLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLE---
                                                                                                                           ; Metazoa;
Eutheria;
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                                                                                                                                                                                                                                                    STANDARD
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                                                                                                                         Chordata;
Primates;
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71.38;
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BY SIMILARITY.
N-LINKED (GLC)
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Pred. No. 4.3e-128;
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CYTOPLASMIC
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                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                    precursor (Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA429F4C6F16E40D CRC64;
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                                                                                                                                                                                       (Glycine
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                                                                                                                           Hominidae;
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VARIANT STHE CYS-307.

VARIANT STHE CYS-307.

Shiang R., Ryan S.G., Zhu Y.-Z., O'Connell P., Wa Shiang R., Ryan S.G., Zhu Y.-Z., O'Connell P., Wa Shiang R., Ryan S.G., Zhu Y.-Z., O'Connell P., Wa Shiang R., Experimental P., Wa Shiang R., Walley R., Walland R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
VARIANTS
                                                                                                                                                                                    MEDLINE=97220600; PubMed=9067762;
Seri M., Bolino A., Galietta L.J.V., Lerone M., Silengo M.,
"Startle disease in an Italian family by mutation (K276E):
subunit of the inhibiting glycine receptor.";
Hum. Mutat. 9:185-187(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation in a family paraparesis.";
J. Med. Genet. 33:43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95072599; PubMed=7981700;
Schorderet D.F., Pescia G., Bernasconi A.,
"An additional family with Startle disease
the alpha 1 subunit of the inhibitory glyci
Hum. Mol. Genet. 3:1201-1201(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Decreased agonist affinity and chloride conductance of mutant glycine receptors associated with human hereditary hyperekplex EMBO J. 13:4223-4228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mutations in the alpha 1 subunit of the inhibitory glycine receptor cause the dominant neurologic disorder, hyperekplexia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS STHE LEU-299 AND GLN-299.
MEDLINE-94129612; PubMed-8298642;
Shlang R., Ryan S.G., Zhu Y.-Z., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96152139; PubMed-8571969; Milani N., Dalpra L., del Prete A., "A novel mutation (266 Gln-->His) i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT STHE CYS-307.

MEDLINE=95336157; PubMed=7611730;

Shiang R., Ryan S.G., Zhu Y.-Z., Fielder T.J.,

Yamashita S., O'Connell P., Wasmuth J.J.;

"Mutational analysis of familial and sporadic

"Monon Neurol. 38:85-91(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION OF STHE POSITION 299 VARIANTS MEDLINE-95009923; PubMed-7925268; Langosch D., Laube B., Runstroem N., Schmieden
   VARIANTS STHE HIS-280 AND HIS-420.
MEDLINE-99442259; PubMed-10514101;
Vergouwe M.N., Tijssen M.A., Peter:
"Hyperekplexia phenotype due to co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elmslie F.V., Hutchings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96311686; PubMed=8733061;
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MEDLINE-95187157; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wasmuth J.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitory glycine-receptor gene (GLRA1)
hyperekplexia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT STHE HIS-294.
MEDLINE-96152139; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (hyperekplexia) caused by mutations inhibitory glycine receptor."; Hum. Mol. Genet. 3:2175-2179(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rees M.I., Andrew M., Ja
"Evidence for recessive
                                                                                                                                                                                                                                                                                                                                                                                VARIANT STHE GLU-304.
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s of GLRA1 in hereditary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        33:435-436(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=7881416;
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as well as dominant
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   Peters A.C.,
to compound
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in the alpha 1 subunit of the
(GLRA1) in hereditary
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or hyperekplexia and spa;
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sease and a Gl192A mutation
glycine receptor gene.";
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, Wielaard R., I
heterozygosity
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   Frants R.R.
y for GLRA1
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                                                                                                                                                                                                                                                               Romeo G.;
the alpha-
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BINDING
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TRANSMEM
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"Novel GLRAI missense mutation (P250T) in domina defines an intracellular determinant of glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000188; GABAA_recepto InterPro; IPR001175; Neur_channel. Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52009; CAA36258.1;
PIR; S12382; S12382.
Genew; HGNC:4326; GLRA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99119431; PubMed=9920650; Saul B., Kuner T., Sobetzko D., E
             VARIANT
                                     VARIANT
                                                             VARIANT
                                                                                   VARIANT
                                                                                                                        CARBOHYD
                                                                                                                                               DISULFID
                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                              Transmembrane;
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                                                                                                            VARIANT
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                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                       MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through
ween the Swiss Institute of Bioinformatics and the Ep
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 SUBUNITS. A THIRD TYPE OF SUBUNIT (93 KI MEMBRANE PROTEIN ASSOCIATED WITH THE CY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN, PARTICULARLY IN THE NEONATAL PERIOD, AND BY AN EXAG
STARTLE RESPONSE TO UNEXPECTED ACOUSTIC OR TACTILE STIMULI.
MISCELLANGOUS: THE ALPHA SUBUNIT BINDS STRYCHNIME.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
DISEASE: DEFECTS IN GLRAI ARE A CAUSE OF HYPEREKFLEXIA
DISEASE (STHE)); AN AUTOSOMAL DOMINANT NEUROLOGIC DISOG
CHARACTERIZED BY MUSCULAR RIGIDITY OF CENTRAL NERVOUS S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE GLYCINE RECEPTOR CHANNEL. BINDING OF GLYCINE TO CONDUCTANCE AND THUS PRODUCES H
                                                                                                                                                                                                                                                                                                                                                                                                138491;
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                                                                                                                                                                                                                                                                                                    ; TIGR00860; LIC; 1.
PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuner T.,
                                                                                                                                                                                                                                                                              Postsynaptic membrane; rane; Multigene family;
                                                                                                                                  248
281
313
337
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2477
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             299
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                                                                                                                                                                                                                                                                                                                                                                         GABAA_receptor.
/FTId=VAR_010112.

R -> H (IN STHE).
/FTId=VAR_010113

Q -> H (IN STHE).
/FTId=VAR_000297

R -> L (IN STHE; D
GLYCINE TO ACTIVAT
                                                                                  N-LINKED (GLCNAC.
I -> N (IN STHE).
/FTId=VAR_000296.
P -> T (IN STHE).
                                                                                                                                  STRYCHNINE (OR
STRYCHNINE (OR
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                      GLYCINE RECEPTOR ALPHA-1 CHAIN
                                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                                                                                            EXTRACELLULAR
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                                                                                                                                                                                                                                                                              Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS A NEUROTRANSMITTER-GATED ION ITS RECEPTOR INCREASES THE CHLORIDE
                                                                                                                                                                                                                                                                                         1. channel;
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STHE; DECREASED ACTIVATE THE CHA
                                                                                                                                                                                                                                                                              mutation
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225)
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Da) IS A PERIPHERAL
TOPLASMIC DOMAINS OF
                                                                                                                                                                                                                                                                                         Glycoprotein;
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                                                                                                                                                          SIMILARITY).
SIMILARITY).
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             POTENCY
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MBL outstation -
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                                                                                                                                                                                                                                                                                         Signal;
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Best Local
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P57695;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-1 chain precursor (Glycine subunit) (Strychnine binding subunit)
             "A nonsense mutation in the alphal subunit of the inhibitory gly receptor associated with bovine myoclonus."; Mol. Cell. Neurosci. 17:354-363(2001).

-I- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED I CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHECONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION NEURONAL FIRING) (BY SIMILARITY).
                                                                                                                                                   Pierce K.D., Handford C.A., Morris Healy P.J., Schofield P.R.;
                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-21109390;
                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                             GLRA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
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   NEURONAL
SUBUNIT:
                                                                                                                                                                                                                                                                                                                           taurus (Bovine).
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                                                                                                                                                                                                                                                                    Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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73.48;
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Pred. No. 3.9e-J
8; Mismatches
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R -> Q (IN STHE; DECREASED POTENCY OF GLYCINE TO ACTIVATE THE CHANNEL).
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/FTId=VAR_010114.
2C6653087B4091B6 CRC64;
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Y -> C (IN STHE).
/FTId=VAR_000301.
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 ALPHA
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kDa) AND
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50;
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                                                                                                                                                                     Dennis J.A.
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                                                                                                                                                                                                                                                                                                                                                                                receptor 48
                                                                                                                              inhibitory glycine
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                                                                                                                                                                                                                                                                                     Bovoidea
(58
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kDa)
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pfam; PF02931; Neur_chan_LBD; 1.
pfam; PF02932; Neur_chan_memb; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: AF268375; AAG14346.1; -.
Interpro; IPR000188; GABAA_receptor.
Interpro; IPR001175; Neur_channel.
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PROSITE; PS00236; NEUROTR_ION_CHANNEL;
Receptor; Postsynaptic membrane; Ionic
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SUBCELLULAR LOCATION: Integral membrane protein.

MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                     351
                                                                        372
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309; Conservative
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                                                                                                            LFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLE
                                   HHKSPMLNLFQEDEAGEGRFNFSAYGMGPACLQAKDGISVKGANNSNTTNP-PPAP-SKS
                                                           RQR------LEEDIIQESRFYFRGYGLG-HCLQARDGGPMEG---SGIYSPQPPAPLLRE
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                                                                                                                                                                                       NTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDAAPARVGLGITTVLT
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BY SIMILARITY.

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STRYCHNINE (OR 225) (
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Pred. No. 4.4e
88; Mismatches
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GLYCINE RECEPTOR ALPHA-1 CHAIN
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    channel; Glycoprotein;

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(BY SIMILARITY).
(BY SIMILARITY).
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycine receptor alpha subunit from zebrafish.";
Neuroscience 90:303-317(1999).
-i- FONCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION
CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLOR
CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                               EMBL; AJ005812; CAA06711.1; ZFIN; ZDB-GENE-991117-1; gl
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Bregestovski P., Korn H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio):
Eukaryota; Metazoa; Chordata; Craniata; Vert
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                                                                                                                                                                        Transmembrane;
SIGNAL
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                                                                                        DOMAIN
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                                                                                                                                              DOMAIN
                                                                                                                                                                                                     Receptor;
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InterPro; IPR001175; Neur_channel.
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15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: HIGHLY SENSITIVE TO ACTIVATION BY TAURINE DESF
THE PRESENCE OF A VALINE IN POSITION 135. IN MAMMALS VALINE A
THIS POSITION CAUSES A DRASTIC LOSS OF TAURINE EFFICACY.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN.
MISCELLANEOUS: THIS RECEPTOR IS ACTIVATED BY GLYCINE ANTAGONIZED BY STRYCHNINE. CAN ALSO BE ACTIVATED BY G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INHIBITED BY BICUCULLINE
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                                                                                                                                                                                                               PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                  Postsynaptic membrane; Ionic
                                                                                                                                                                                                                               TIGR00860; LIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                       Multigene
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STRYCHNINE (OR 22)
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GLYCINE RECEPTOR,
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zebrafish.";
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channel;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-1 chain precursor (Glycine
Identification and chromosomal localization of a J. Biol. Chem. 269:2607-2612(1994).

1. FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRAN CHANGEL BINDING OF GLYCINE TO ITS RECEPTOR I CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATI NEURONAL FIRING.

1. SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) SUBUNITS A THIRD TYPE OF SUBUNIT (93 kDa) IS MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLAS
                                                                                                                                                                                                                                                                                                                                                                                                                    Ryan S.G., Buckwalter M.S., Lynch J.W., Handford C.,
Shiang R., Wasmuth J.J., Camper S.A., Schofield P.,
"A missense mutation in the gene encoding the alpha
inhibitory glycine receptor in the spasmodic mouse."
Nat. Genet. 7:131-135(1994).
                                                                                                                                                                                                                                                                  Guenet J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammaalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subunit) (Strychnine binding subunit).
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                                                                                                                                                                                                                                                                                          Matzenbach B., Maulet Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., MEDLINE=95004575; P
                                                                                                                                                                                                           "Structural analysis of mouse glycine receptor alpha subunit genes. Identification and chromosomal localization of a novel variant.";
                                                                                                                                                                                                                                                                                                                     MEDLINE=94132024; PubMed=7507926;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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InterPro; IPR000188; GABAA_recepto
InterPro; IPR001175; Neur_channel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                  TRANSMEM
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SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND ALTERNATIVE SPLICING.

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPASMODIC (SPD), A MOU DISEASE; DEFECTS IN GLRA1 ARE A CAUSE OF SPASMODIC (SPD), A MOU MUTANT WHICH RESEMBLES TO THE HUAUSE OF SPASMODIC AND MUTANT WHICH RESEMBLES TO THE LIGAND STRYCHNINE.

HYPEREKPLEXIA (OR STARTLE DISEASE (STHE)).

MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.

SIMILARITY: BELONGS TO THE LIGAND GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinformatics 
European Bioinformatics Institute. There a 
by non-profit institutions as long as i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF02931; Neur_chan_LBD; 1.
PF02932; Neur_chan_memb; 1.
S; PR00252; NRIONCHANNEL.
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GLYCINE RECEPT
EXTRACELLULAR
                                             Score 1569.5; I
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BY STMILARITY.

N-LINKED (GLCNAC. . ) (PROBABLE).

STRYCHNINE (OR 230) (BY SIMILARITY).

STRYCHNINE (OR 225) (BY SIMILARITY).

MISSING (IN SHORT ISOFORM).
                                                                                          A -> S (IN SPD).
M -> I (IN REF. 2).
ISRI -> NISH (IN REF.
29268DC4991A6E20 CR
                                                                                                                                                                                                                                                               PROBABLE.
CYTOPLASMIC
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                                Mismatches
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MEDITINE-91367372; PubMed-1716350;
MEDITINE-91367372; PubMed-1716350;
Akagi H., Hirai K., Hishinuma F.;
Akagi H., Hirai K., Hishinuma F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor alpha-1 chain precursor (Gly
subunit) (Strychnine binding subunit).
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STRYCHNINE BINDING SITE.
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                                            Sontheimer H., Becker C.M., Prito
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Neuron 2:1491-1497(1989).
                                                                                                                                                                                Grenningloh G., Rienitz A., Schmitt B., Methfessel C., Zensen Beyreuther K., Gundelfinger E.D., Betz H., Betz H., "The strychnine-binding subunit of the glycine receptor shows homology with nicotinic acetylcholine receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                              MEDLINE=87258250;
                                                                                                                      MEDLINE=90180468; PubMed=2483325;
                                                                                                                                                                                                                                                                            SEQUENCE OF 23-457 FROM N.A. (SHORT ISOFORM), AND
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 WKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCT
                                                                                                                                                                     328:215-220(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCC
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                                                                                                                                                                                                                                                                                                        in Xenopus oocytes injected Res. 11:28-40(1991).
                                                                                                                                      1-30 FROM
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Hishinuma F.;
                                                                                                                                                                                                                                              PubMed=3037383;
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                                                                                        Pritchett D.B.,
H., Betz H., See
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Sciurognathi;
                                                                           Betz H., See
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thi; Muridae; Murinae; Rat
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                                                                                                        Schofield P.R.,
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                                                                                                                                                                                                                                 Zensen M.,
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                                                                             rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Localization of the
subunit of the glycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1. PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malosio M.L., Grenningloh Prior P., Betz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry
                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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MEDLINE-91115810; PubMed-1703526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mayor F.
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                                                                                                           CONFLICT
                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the inhibitory glycine receptor.";

Biol. Chem. 266:2048-2053(1991).

- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION

CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLON

CHANNEL. BINDING OF GLYCINE TO THE RECEPTOR INCREASES THE CHLON

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CHANNEL BINDING OF GLYCINE THE PROPERTY OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN H
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
MISCELLANEOUS: THE ALPHA SUBUNIT BINDS STRYCHNINE.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: PENTAMÉR COMPOSED OF ALPHA (48 kDa) AND BETA (58 ) SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR CORE
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JN0014; JN0014
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000188; GABAA_receptor.
IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                     Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR00860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the glycine receptor. ry 29:7033-7040(1990).
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                                                                             STRYCHNINE (OR 230).
STRYCHNINE (OR 230).
STRYCHNINE (OR 225).
MISSING (IN SHORT ISOFORM).
MYSENTLRFYLWETIVFFSLAA -> MG
LFEFP (IN REF. 3).
A -> V / YN REF.
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Pred.
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                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                                                                                                                                             PROBABLE
                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                  GLYCINE RECEPTOR
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                                                    -> V (IN REF. 2).
0379C33A83C71FAA
                                                                                                                                                                                                                                                                                                                                                                                  Alternative
                                                                                                                                                                                                                                                                                                                                                                                                      Ionic
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1568.5; DB 1;
No. 4.2e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                     channel;
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                                                                                                                                                                                                                                                        (PROBABLE)
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P48168;
01-FEB-1996 (Rel. 33, 0)
01-FEB-1996 (Rel. 33, 1)
15-JUN-2002 (Rel. 41, 1)
Glycine receptor beta
                                                         Guenet J.-L., Kubse J., Betz H., Becker C.M.;
"The spastic mouse: aberrant splicing of glycine subunit mRNA caused by intronic insertion of L1 e Neuron 13:1003-1015(194).

-!- FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRAN
                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS SPASTIC. STRAIN=C57BL/6, and BALB/c; TISSUE=Brain, MEDLINE=95033198; PubMed=7946325;
 + +
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        GLRB.
                                                                                                                                                                                                                                                                                                                                                 subunit).
                                                                                                                    Muelhardt
                                                                                                                                                                                           associated with
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                                                                                                                                                                                                                              Kingsmore S.F.,
                                                                                                                                                                                                                                            MEDLINE=95004576;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                      'Glycine receptor beta-subunit
NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED
SUBCELLULAR LOCATION: Integ
                                  FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSPEEMRKLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKPDLFFANEKGAHFHEITTDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMDVQTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPVNVSCNIFINSFGSTAETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSI
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                                                                                                                                                                                                                                                                                                  Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                               with LINE-1 element
7:136-141(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                         (Mouse)
                                                                                                                    Fischer M., Gass P.,
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                              Giros
                                                                                                                                                                                                                                                                                                                                                                    . 33, Created)
. 33, Last sequence.
. 41, Last annotation.
                                                                                                                                                                                                                                        PubMed=7920630;
                                                                                                                                                                                                                                                                                                           Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417
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B
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                                                                                                                                                                                                                                                                                                                                                              chain
Integral
                                                                                                                                                                                                                              Suh D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·SFGYTMNDLIFEWQEQG-AVQVADGLTLPQFILKEEKDLRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                             precursor
                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
            OF.
                                                                                                                                                                                           insertion
                                                                                                                                                                                                      gene
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             ALPHA AND
                                                                                                                                                                                                                              Bieniarz M.,
                                                                                                                   Simon-Chazottes
membrane
                                                                                                                                                                                                      mutation
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(Glycine
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             BETA
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                                                                                                                                             Liver;
                                                                                                                                                                                                                                                                                                                                                             receptor
                                                                                                                                                                                                                              Caron M.G.,
                                                                                   element.
                                                                                                                                                                                                      spastic mouse
                                                                                    receptor
element.";
             SUBUNITS
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                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                              beta
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8
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Best Local
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DISULFID
CARBOHYD
CARBOHYD
VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L32594; AAA65966.1; MGD; MGI:95751; Glrb.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U09399; AAA61874.1; -. EMBL; X81202; CAA57076.1; -. EMBL; X81201; CAA57075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIPPOCAMPUS, THALAMUS AND CEREBELLUM.

DISEASE: DEFECTS IN GLRB CAUSE THE SPASTIC CONDITION WHICH CHARACTERIZED BY MUSCLE RIGIDITY, TREMORS, MYOCLONIC JERKS, PRONOUNCED STARTLE REACTION, ABNORMAL GAIT AND IMPAIRED RIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: HIGH LEVELS OF EXPRESSION IN CORTEX.
                                                                                                             178
                                                                                                                                                167
                                                                                                                                                                                    120
                                                                                                                                                                                                                       801
   285
                                                                         227
                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                              188;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                         -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL 166
                                                                                                                                                                                                                                                                                            LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit
                                      L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                             SITLSCPLDLTLFPMDTQRCKMQLE----
                                                                                                                                              TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                   LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ-------PMSPSDFLDK
                                                                                                                                                                                                                                                          LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                   ISFFILMSL----LFEDACAKEKSSKKGKKKQYLCPSQQSPEDLARVPPNSTSNILNR
ILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR00860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Disease mutation.
BY 2
BY 2
23 496 GLY
23 265 EXTI
29 PROD
31 PROD
31 PROD
31 CYTC
21 CYTC
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151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WE;
                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 871; DB 1; Pred. No. 1.3e-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN SPASTIC 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (PROBABLE). PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFFANEKSA -> VSMSWIYNR (IN SPASTIC 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN SPASTIC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFKGIPVDVV -> TTMLDIQPMI (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 555FDFA8918437BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR BETA CHAIN LULAR (PROBABLE)

    channel; Glycoprotein; Signal;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage by
                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 496
                                                                                                           SFGYTTDDLRFIWQSGDP-VQ
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                                                                                                                                                                                                                                                                                                                                                                                                        52;
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                                                                                       Matches
                                                                                                     Query Match
Best Local
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-j- SIMILARITY: BELONGS TO 7
PIR; JH0165; JH0165.
Interpro; IPR000188; GABAA_]
Interpro; IPR001175; Neur_cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991
01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRB_RAT P20781;
                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycine receptor beta chain precursor (Glycine receptor 58 kDa
                                                                                                                                                                              TRANSMEM DISULFID
                                                                                                                                                                                                                                                                                                      TIGKEAMS; LIBROUGUS, NEUROTR_ION_CHANNEL; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Constaurablic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycine receptor.";
Neuron 4:963-970(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90297968;
Grenningloh G., Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE-90297968; PubMed-2163264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subunit).
                                                                                                                                                                                                                                                                                                                                     TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                 Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taleb O., Betz H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and expression of the 58 kd beta subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA (48 kDa) AND BETA (58 kDa) SUBUNITS. A THIRD TYPE OF SUBUNIT (93 kDa) IS A PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH THE CYTOPLASMIC DOMAINS OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THE GLYCINE RECEPTOR IS A NEUROTRANSMITTER-GATED ION CHANNEL. BINDING OF GLYCINE TO ITS RECEPTOR INCREASES THE CHLORIDE CONDUCTANCE AND THUS PRODUCES HYPERPOLARIZATION (INHIBITION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 ASLVEYAVVQVMLNNPK---RVEAEKRR 366
                                                                                         187;
             51
                                        7
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                                                                                                                                                                                                                                                                                                                                                    PR00252;
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                     VSFFILMSL ---- LFEDACSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPPNSTSNILNR
                                                              LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALLEYAAINEVSROHKEFIRLRRRORR
                                                                                                                                                                                                                                                                                                                                        TIGR00860; LIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 17, Created)
                                                                                         Conservative
                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pribilla
NRIONCHANNEL.
                                                                                                                                         242
55927
                                                                                                                                                                   22
496
265
290
316
316
477
495
197
                                                                                                     38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      GABAA_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                 N: Integral membrane TO THE LIGAND-GATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ι.,
                                                                                                                                           X.
                                                                                                                                                                                                                                                                                                                                                                                          channel.
                                                                                         63;
                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; F77CE96105EF8ACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prior P., Multhaup G.,
                                                                                                     Pred
                                                                                                                Score 863.5;
                                                                                                                                                                              PROBABLE.
BY SIMILARITY
                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                     PROBABLE
                                                                                                                                                                                                                                  PROBABLE.
                                                                                                                                                                                                                                               PROBABLE
                                                                                                                                                                                                                                                         EXTRACELLULAR
                                                                                                                                                                                                                                                                       GLYCINE RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                       Mismatches
No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372
                                                                                     5.7e-66;
hes 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                       (PROBABLE)
                                                                                                                DB 1;
                                                                                                                                                                                                                                                         (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
IONIC CHANNEL FAMILY
                                                                                       Indels
                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beyreuther
                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAINS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the inhibitory
                                                                                                                 496;
                                                              - PMSPSDFLDK
                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                              Signal
                                                                                       Gaps
                                                               50
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              107
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RESULT 13
GRB_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRB_HUMAN P48167;
                                                                                                                                                                  01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-JUN-2002 (Rel. 41,
Glycine receptor beta
                                use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                 the
                                                                                                                                                                                                                                           MEDLINE-98341117; PubMed-9676428;
Milani N., Muelhardt C., Weber R.G., Lichter P., Kioschis
Poustka A., Becker C.-M.;
                                                                                                                                                                                                                                                                                                     Brain
                                                                                                                                                                                                                                                                                                                  and murine
                                                                                                                                                                                                                                                                                                                          Handford C.A., Lynch J.W., Baker E., Sutherland G.R., Schofield P.R.; "The human glycine receptor beta subtfunctional characterisation and chron
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Hippocampus;
MEDLINE=96352561; PubMed=8717357;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                            SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO THE LIGAND-GATED
                                                                               European
                                                                                                                                                   NEURONAL FIRING).
SUBUNIT: PENTAMER COMPOSED OF ALPHA AND BETA SUBUNITS
                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345
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                                                                                                                                                                                                                                                                                                    Res. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASLVEYAVVQVMLNNPKRVEAEKARIAKAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALLEYAAI - - - - NEVSRQHKEFIRLRRRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITLSCPLDLTLFPMDTQRCKMQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                      ,s (Human).
Metazoa; Chordata; C
™..+heria; Primates; (
                                                                                                                                                                                                                                                                                                                genes.";
            AAB37750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                     Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
Last annotation
chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                     Res.
                                                                                                                                                                                                                                                                                                     35:211-219(1996)
                                                                                                                                                                                                                                                                                                                           beta subunit: pand chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                            Webb G.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
(Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                                                                                                                                                                                                     primary
                                                                   as its content
                                           http://www.isb-sib.ch/announce/
                                                                                                                            protein.
IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                            localisation
                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
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                                                        bу
                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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Best Local S
Matches 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; Trum.
TIGREAMS; Trum.
Therefore PS00236; Northerefore
                                                                                                                            GAB_LYMST P26714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM TRANSMEM
                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Gamma-aminobutyric-acid receptor beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                         01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02931; Neur_chan_LBD;
Pfam; PF02932; Neur_chan_memb;
PRINTS; PR00252; NRIONCHANNEL.
SEQUENCE
                                Eukaryota; Metazoa;
Lymnaeidae; Lymnaea
                                                       Lymnaea stagnalis (Great pond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000188; GABAA_receptor
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 138492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF094755; AAC71034.1; Genew; HGNC:4329; GLRB.
                     NCBI_TaxID=6523;
                                                                    receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 38.0%;
Similarity 47.4%;
86; Conservative (
                                                                                                                                                                                                                                                                                                     QVAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLI
|: | : ||| | ::: : | |||:| || :||:|| | | ||:|::: : | |:|||
                                                                                                                                                                                                                                                                                                                                                                                                                                             KLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAFLILISL----WVEEAYSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPANSTSNILN
FROM
                                                                                                                                                                                                                                                                 VILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFV
                                                                                                                                                                                                                                                                                                                                                            LTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAV
                                                                                                                                                                                                                                                                                                                                                                                    PSDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMR
                                                                                                                                                                                                                                                                                                                                                                                                          --SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                 RLL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM-----
                                                                                                                                                                                                FASLVEYAVVQVMLNNPKRVEAEKARTAKAEQ
                                                                                                                                                                                                                      FAALLEYAAI ----NFVSRQHKEFIRLRRRQR
                                                                                                                                                                                                                                             VVLSWLSFWINPDASAARVPLGIFSVLSLASECTTLAAELPKVSYVKALDVWLIACLLFG
                                                                                                                                                                                                                                                                                        QL-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLI
                                                                                                                                                                                                                                                                                                                                     LSITLSCPLDLTLFPMDTQRCKMQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR00860; LIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
497
N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
497
265
290
316
354
478
478
496
197
197
242
56122
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                                             Mollusca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 855 5; DB pred. No. 2.7e-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
C1F0B407601D3625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
GLYCINE RECEPTOR BETA CHAIN
                                           snail).
Gastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 2.7
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ionic
                                                                                                                                        499

    channel; Glycoprotein; Signal;

                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROBABLE)
                                                                                                                                                                                               372
                                                                                                                                                                                                                      371
                                             Pulmonata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 68
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-SFGYTTDDLRFIWQSGDP-V

225 176

283

280

Indels Length 497;

53

SPSDFLD Gaps

61

107

precursor

(GABA(A)

Basommatophora;

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Best Local S
Matches 146
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PIR; S17785; S17785.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
DISULFID
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CARBOHYD
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DOMAIN
TRANSMEM
CARBOHYD
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harvey R.J., Vreugdenhil E., Zaman S.H., Bhandal N.S., Usherwood P.N.R., Barnard E.A., Darlison M.G.; "Sequence of a functional invertebrate GABAA receptor can form a chimeric receptor with a vertebrate alpha s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Postsynaptic membrane; Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHANNEL.
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00236; NEUROTR_ION_CHANNEL;
                         NGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVF
                                                                                                                                                                                                                                            : ::|||| : |::| | : |::| | : |::| || : |::| || : |::| || : |::| || : |::| || : |::| || : |::| || : |::| || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
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                                                                                                         EWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQM
                                                                                                                                                                NGSLYYGMRFTTTLACMMDLHNYPLDHQECTVEIE--
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
.3e-55;
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(POTENTIAL).
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RESULT 15
GAB4_CHICK
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-i- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERTEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO TO GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bateson A.N., Lasham A., Darlison M.G.; "Gamma-aminobutyric acid A receptor heterogeneity is increased alternative splicing of a novel beta-subunit gene transcript."; J. Neurochem. 56:1437-1440(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Gamma-aminobutyric-acid receptor beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X56647; CAA39969.1;
EMBL; X56648; CAA39970.1;
PIR; JH0360; JH0360.
PIR; JH0359; JH0359.
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          CARBOHYD
                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                          Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Multigene family; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00252; NRIONCHANNEL. TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHANNEL.
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES RECEPTOR CHAINS: ALPHA, BETA, GANMA, DELTA, AND RHO. SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-4 AND BETA-4
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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     PROBABLE.
N-LINKED
N-LINKED
N-LINKED
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                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                EXTRACELLULAR
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(POTENTIAL).
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| Sea: Job | Оγ | ОУ | ОУ | Db Qq | pb Qy | рь | pb dy | X B O | FT FT SQ |
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| rch completed: June 2 time : 19.3557 secs | 383 368 | 335 308 | 275 248 | 215 . 189 | 155 143 | 95 84 | 43 27 | Query Match Best Local : Matches 156 | CARBOHYD DISULFID VARSPLIC SEQUENCE |
| Search completed: June 25, 2003, 17:15:56 Job time : 19.3557 secs' | SRFYFRGYGLGHCLG | WMAVCLLEVFAALLEYAAINEV :: : YLMGCFVFVFLALLEYAFVNYI | QMYIPSLLIVILSWV : : QTYMPSILITILSWV | VFEWLEDAPAVQVAE | FKNGNVLYSIRLTLI : : : HPDGTVLYGLRITTI | NVFLRQQWNDPRLSYREYP :: : : : TMYFQQSWRDKRLAYNDLP | SPSDFLE | Query Match Best Local Similarity 38.0 Matches 156; Conservative | 195 195 160 174 361 364 488 AA; 5606 |
| 003, 17:15:56 | SRFYFRGYGLGHCLQARDGGPMEGSGIYSPQPPAPLLREG 422 : : | WMAVCLLEVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQE :: : | QMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDI | VFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEVKFHLERQMGYYLI | FKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTNKDL | NVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRI::: | SPSDELDKLMGRTSGYDARIRPNEKGPPVNVTCNIEINSESSVTKTTMDYRV | 32.2%; Score 726; DB 1; Length 488; 38.0%; Pred. No. 2.9e-54; Indels 52; Gaps ive 79; Mismatches 124; Indels 52; Gaps | 95 N-LINKED (GLCNAC) (POTENTIAL). 74 BY SIMILARITY. 64 MISSING (IN ISOFORM BETA-4). 56068 MW; 164A75314BDB2C12 CRC64; |
| | | 367 | 334 | 274 | 188 | 154 | 83 | 10; | |

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Result
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                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1886
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                                                                                                                                                                                                                                                                                                                  SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_inverteb
6: sp_mammal:*
5: sp_mhc:*
8: sp_organel:
9: sp_mhage:*
10: sp_phage:*
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
14: sp_urclass
15: sp_virus:*
16: sp_bacteri
17: sp_archeap
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length: 2000000000
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2252
1 MTTLVPATLSFLL
                                                                                                                                                                                                           Match
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Gapop 10.0 ,
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69.1
68.3
61.3
38.9
37.8
33.2
33.2
33.0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_bacteria:*
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sp_archeap:*
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sp_rvirus:*
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   5 5 5 5 6 1 1 3 1 3
                       Q8VHF3
Q9DES9
Q99LS9
Q91XP5
Q9GKF0
Q9GKF0
Q9GKB9
Q8QG93
Q9QW13
Q9OW13
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1705.612 Million cell updates/sec
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Oddy93 brachydanio
O90w14 brachydanio
O90w13 brachydanio
O9des8 brachydanio
O9des8 brachydanio
O9dy159 bos taurus
O9dy14 sepia offic
O46124 haemonchus
O77295 drosophila
O94900 drosophila
O94900 drosophila
O96773 lucilia cup
                                                                                                                    Q9gkf0 bos taurus
Q9gke9 bos taurus
                                                                                                                                                                                                         Description
                                                                                                                                                    Q8vhf3 mus musculu
Q9des9 brachydanio
Q99jc9 rattus norv
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ALIGNMENTS

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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 358; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-B6C3/FE; TISSUE=SPINAL CORD;
Groemer T.-W.W., Becker C.-M.M., Becker K.;
"Localization of different glycine receptor isoforms in murine spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8VHF3 PRELIMINARY; PRT; 416 AA.
Q8VHF3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alpha 4 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRPAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF462147; AAL69899.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cord."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRA4
416 AA;
                                                                                                                                                                      83.7%; Score 1886; DB 11; llarity 91.8%; Pred. No. 3.7e-169; Conservative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                    48322 MW; C095998F4C077451 CRC64;
                                                                                                                                                                                                                                                     Length 416;
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Query Match
Best Local S
Matches 334
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Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alphaz2 subunit.
GLRA4A OR GLRA2 OR GLYR ALPHA.
Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DES9
Q9DES9;
01-MAR-2001
                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ404970; CAC16687.1;
ZFIN; ZDB-GENE-010410-3; g1ra4a.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                      Bregestovski P.;
"Isolation and Characterization of a alpha 2-type zebrafish Receptor Subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imboden M., de Saint Jan D., Leulier F., Korn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
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                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVFAALLEYAAINFVSRQHKEFIRLRRRQRRQRLEEDIIQESRFYFRGYGLGHCLQARDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVL
                                                                 LCFLYLW--
                                                                                                                                                                                                                        PS00236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVFAALLEYAAVNFVSRQHKEFMRLRRRQRRQRMEEDIIRESRFYFRGYGLGHCLQARDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSIRLTLILSCPMDLKNEPMDIQTCTMQLE------SEGYTMNDLMFEWLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNDPRLAYREYPDDSLDLNPSMLESIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVL
                                                                                                                                                                                          456
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                          AA;
                                                                                                                                                                                                                       NEUROTR_ION_CHANNEL;
                                                                                                                                                                                          52674 MW;
                                                                                                                          77.7%; Score 1749.5; 78.8%; Pred. No. 3.16 tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                        62713B7F29999FBD CRC64;
                                                                                                                          9.5; DB 13; Length
3.1e-156;
ches 25; Indels
                                                              -QKPMSPSDFLDKLMGRTSGYDARIRPNFKG
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                                128
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                                                                                                                                                          Matches
                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                              "Concentration dependence of single channel currents the recombinant alpha 1 glycine receptors.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY -- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNE EMBL; AJJ310838; CAC35982.1;
Interpro: IDDONN'100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99JC9 PRELIMINARY;
Q99JC9;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                             pfam; pF02931; Neur_chan_LBD; 1.
pfam; pF02932; Neur_chan_memb; 1.
prints; pR01520; GABAARGAMAA.
prints; pR00552; NRIONCHANNEL.
TIGREMMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                  Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                TIGREAMS; TIGRO0860; LIC; 1. PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; Beato M., Groot-Kormelink P.J., Colquhoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycine receptor alpha
                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                     Transmembrane.
                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                              84
                                                             69
                                                                                             27
                                                                                                                          9
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQRRQRLEEDIIQESR-FYFRGYGLGHCLQARDGGPMEGSGIYSPQPPAPLLREGETTRK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLE-----SFGYTMNDLIFEWLSDNP-VQVADDLTLPQFVLKEEKDLGYCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYVD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLIVFAALLEYAAVNFVSRQHKEFIRLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTM
KPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTM
                              PPVNVTCNIFINSFGSIAETTMDYRVNIFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKDGTAVEGSSVFAPPPPVQVLYDGEAVRK
                                                                                                                                                                                                                     480 AA;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                     55555 MW;
                                                                                                                                                                     71.0%;
                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                      Score 1598; DB 11;
Pred. No. 6.2e-142;
                                                                                                                                                                                                                     322478D9A3052299 CRC64;
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   currents through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                        Indels
                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                         CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat
                                                                                                                                                      Gaps
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밁 8

188

143

83

В Ş

204

304

244

364 376

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Q91XP5;
Q91XP5;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Glycine receptor alpha 3 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SPINAL CORD;
Noegel S., Becker C., Becker K.;
"Different glycine receptor isoforms cerebellum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02931; Neur_chan_EBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR01620; GABAARGAMMA.
TIGREAMS; TIGR0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF362764; AAK51962.1; -. MGD; MGI:95749; G1ra3. InterPro; IPR000188; GABAA_receptor. InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                     Local L
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLTWTTQSSGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINFVSRQHKEFIRLRR 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPPAPLLREGETTRKLYVD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSSYTKTTMDYRVNYFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN 141
                                                                                                                                                                                                                                                   LLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHYNTGKFTCIEVRFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITT
SLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEV
                                                                                                                                                                                                                              LLLSLVATKETNSARSRSAPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----MPKSADEMRKVFID
                                                                                                                                                                                                                                                                                                                                                                                                             463 AA;
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               53605 MW;
                                                                                                                                                                                                                                                                                                                                           70.1%;
73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFGYTMNDLIFEWQDEAP-VQVAEGLTLPQFLLKEEKDLRYCT
                                                                                                                                                                                                                                                                                                                        33
'
                                                                                                                                                                                                                                                                                                                   Score 1578; DB 11;
Pred. No. 4.5e-140;
33; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoforms are expressed in murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             889D67DE9B223605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .308
                                                                                                                                      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
  261
                                               189
                                                                                       201
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Q9GKF0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                            Query Match
Best Local S
Matches 307
                                                                                                                                                                                                                                                                                                          EMBL; AF268365; AAG41140.1; JOINED.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF268366; AAG41140.1; JOINED EMBL; AF268358; AAG41140.1; JOINED EMBL; AF268359; AAG41140.1; JOINED EMBL; AF268369; AAG41140.1; JOINED EMBL; AF268361; AAG41140.1; JOINED EMBL; AF268362; AAG41140.1; JOINED EMBL; AF268363; AAG41140.1; JOINED EMBL; AF268363; AAG41140.1; JOINED EMBL; AF268365; AAG41140.1; AAG41140.1; AAG41140.1; AAG41140.1; AAG41140.1; AAG41140.1
                                                                                                                                                                                                    Glycoprotein; Ic
Transmembrane.
SEQUENCE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alpha 1 subunit isoform b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GKF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierce K.D., Handford C.A., Morris R., Vafa B
Healy P.J., Schofield P.R.;
"A nonsense mutation in the alphal subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLRA1
                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor associated with bovine myoclonus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GKF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21109390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell. Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
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                                                                                                                 307; Conser
                                                                  12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVALGITTDLTMTTQSSGSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SFGYTMNDLIFEMQDEAP-VQVAEGLTLPQFLLKEEKDLRYCTKHYNTGKFTCIEV
                                            RKVFID 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYRFSDTDDEVRESRFSFTAYGMGPCLQAKDGVVPKGPNHAVQV---MPKSP-----DEM 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLPKVSYVKAIDIWMAVCLLEVESALLEYAAVNEVSROHKELLRERRKRKNKTEAFALEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKEFIRLRRRQRRQ----RLE-
                       LYLWE----TIVFFSLAASKEAEAARSASKPMSPSDFLDKLMGRTSGYDARIRPNFKGPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EDIIQESRFYFRGYGLGHCLQARDG----GPMEGSGIYSPQPPAPLLREGETT 425
                                                                                                            69.7%;
ilarity 72.6%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                 Ionic
                                                                                                                                                                                                      AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11178872;
                                                                                                                                                                                                                                              channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                      51676 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17:354-363(2001)
                                                                                                            Score 1570; DB 6;
Pred. No. 2.5e-139;
7; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                      DC75FB56F3114A4C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B., Dennis J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                      CRC64;
                                                                                                                                                       Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibitory
                                                                                                               26;
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                                                                                                            Gaps
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GLRA3

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426 413 369

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Query Match Best Local Matches

Receptor. SEQUENCE

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                                                                                -1- SUBCELLULAR LOCATION: INVEGRAL MEMBRANE PRO
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED ION
EMBL; AF268356; AAG41141.1; JOINED
EMBL; AF268359; AAG41141.1; JOINED
EMBL; AF268359; AAG41141.1; JOINED
EMBL; AF268360; AAG41141.1; JOINED
EMBL; AF268361; AAG41141.1; JOINED
EMBL; AF268362; AAG41141.1; JOINED
EMBL; AF268362; AAG41141.1; JOINED
EMBL; AF268363; AAG41141.1; JOINED
EMBL; AF268363; AAG41141.1; JOINED
EMBL; AF268365; AAG41141.1; JOINED
EMBL; AF268365; AAG41141.1; JOINED
INTERPRO; IPRO00188; GABAA, receptor.
InterPro; IPRO01175; Neur_chan_e1.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFINTS; PR01620; GABAARGAMMA.
PRINTS; PR01
                                                              Glycoprotein; Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A nonsense mutation in the alphal subunit of the inhibitory receptor associated with bovine myoclonus."; Mol. Cell. Neurosci. 17:354-363(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paccess PubMed=11178872; Pierce K.D., Handford C.A., Morris Healy P.J., Schofield P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alpha 1 subunit isoform a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GKE9;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-21109390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
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   AA;
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   MW.
                                                                  Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
F31C41BFC8786908
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IONIC CHANNELS FAMILY.
CRC64;
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cora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.A.
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RESULT 7

Q80693
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Best Local S
Matches 307
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PRELIMINARY; PRT; 459 AA.

O8QG93;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLEL 21, Last annotation update)
Glycine receptor alphazl. subunit.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euchtopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL/GenBank/DDBJ EMBL, AF488379; AAM00910.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Devignot V., Prado de Carvalho L., Bregestovski P.,
"A Novel Glycine Receptor aZl Subunit Variant in the
Brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409
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307; Conserv
                                                                                                                                       12 LLLWTLPGQVLLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPNFKGPPV
                                                                                                                                                                                                                                                  Similarity
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QGSKSDGTHKKGPPVNVTCNIFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYSEYPDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HHKSPMLNLFQEDEAGEGRFNFSAYGMGPACLQAKDGISVKGANNSNTTNP-PPAP-SKS
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                                                                                                             IYLW----ETIVFFSLAASQQAAARKAASPMPPSEFLDKLMGKVSGYDARIRPNFKVVDP
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                                                                                                                                                                                                                                                                                                                                      459
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                                                                                                                                                                                                                                                                                                                                      AA;
                         -KGPPVNVTCNIFINSESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430
                                                                                                                                                                                                                                                                                                                                   52330 MW;
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                                                                                                                                                                                                                                               Pred.
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Pred. No. 2.5e-139;
                                                                                                                                                                                                                                                                         Score 1555.5;
                                                                                                                                                                                                                                                                                                                                   FFC97E289FA3404A CRC64
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                                                                                                                                                                                                                                                  NO.
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Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                  .9e-1
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121
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RESULT OPEN ACCORD DE COMMENT OF THE COMMENT OF THE
                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 301; Conser
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O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor alphaz3 subunit precursor.
GLRA3 OR GLYRALPHA3.
                                                                                                                                                                                                                                                                                                                                                                                              Imboden M., Devignot V., Goblet C.;

"Phylogenetic relationships and chromosomal location of five distinct glycine receptor subunit genes in the teleost danio rerio.";

Dev. Genes Evol. 211:415-422(2001).

EMBL: AJ308516; CAC38837.1;

EFIN: ZDB-GENE-020402-1; glra3.

InterPro: IPR000188; GABAA_receptor.

InterPro: IPR000188; GABAA_receptor.

InterPro: IPR001175; Neur_channel.

Pfam: PF02931; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                               CHAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1620; GABAARGAMMA.
TIGREAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21541038; PubMed=11685575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                       Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                ARQHKELLREQR--RRRHLKEDEAGDGRESFAAYGMGPACLQAKDGMAIKGNNNNAPTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDL
                                       ESSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANEKGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPPEKTVEEMRKLFI 419
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                    FGSIAETTMDYRVNIFLRQKWNDPRLAYSEYPDDSLDLDPSMLDSIWKPDLFFANEKGAH
                                                                                                                                                                                                                                                               28
450 A
                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                            27 F
450 G
51636 MW;
                                                                                                                                                                                                    68.3%;
72.9%;
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                                                                                                                                                                                 33;
                                                                                                                                                                             Score 1537.5;
Pred. No. 2.9e
33; Mismatches
                                                                                                                                                                                                                                                               GLYCINE RECEPTOR ALPHAZ3 SUBUNIT; FDD64C009EF60EA0 CRC64;
                                                                                                                                                                                                                                                                                                      POTENTIAL
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les 54;
                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                 Indels
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Best Local
                                                                                                                                                                                                                                                                                                      Matches
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Q90WT3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-ycine receptor alpha24 subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic relationships and chromosomal location of five distinct glycine receptor subunit genes in the teleost danio rerio.";

Dev. Genes Evol. 21:415-422(2001).

EMBL; AJ308517; CAC38838.1;

ZFIN; ZDB-GENE-020402-2; glra4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02931; Neur_chan_LBD; 1. Pfam; PF02932; Neur_chan_memb; 1 TIGRFAMS; TIGR0860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21541038; PubMed=11685575;
Imboden M., Devignot V., Goblet C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLRA4B OR GLYRALPHA4
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000188; GABAA_receptor
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                            GPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSI
                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGITTVLTMTTOSSGSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGCCTKHYNTGKFTCIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLP
                    TKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARVGLGIT
                                                                             GPPVNVTCNIFINSFGSITETTMDYRLNVFLRQQWNDPRLAYKEYPDDSLDLDPSMLDSI
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                                                                                                                                         WKPDLFFANEKGANFHEVTTDNKLLRIFQNGNVLYSIRLTLILSCPMDLKNFPMDTQTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESRLSFTPNA-----GKDGAVPKTANNAATTPSEPAVAPGKSHEEMRKLFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESRFYFRGYGLGHCLQARDGGPMEGSGIYSPQPPAPLLREG---ETTRKLYVD
                                                            VQLE-----
426 AA;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SFGYTMNDLIFEWQEKGP-VQVADGLTLPQFILKDESDLRYCTKHYNTGKFTCIEV
                                                                                                                                                                                                                                                                                                                                                                               1
48503 MW;
                                                                                                                                                                                                                                                                                                                       61.3%;
67.7%;
                                                                                                                                                                                                                                                                                                    31;
                                                          SEGYTMNDLIEQWLDEGP-VQVADDLMLPQEVLKEEKDLGYC
                                                                                                                                                                                                                                                                                                                     Score 1381; DB 13; Pred. No. 1.5e-121;
                                                                                                                                                                                                                                                                                                                                                                                 9187E20B8793234B CRC64;
                                                                                                                                                                                                                                                                                                      Mismatches
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Best Local S
Matches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DES8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glycine receptor betaZ subunit precursor (Fragment).
GLRB OR GLYR BETA. (Tabrafish) (Tabra danio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regional Passin,";
System of Zebrafish.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCÁTION: INTEGRÁL MEMBRANE
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED
EMBL AJ404971; CAC15688.1; -
ZFIN: ZDB-GENE-010410-2; glrb.
InterPro; IPR000188; GABAA_receptor
InterPro; IPR0001175; Neur_chan_el.
pfam; PF02931; Neur_chan_LED; 1.
pfam; PF02931; Neur_chan_LeD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygli; Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DES8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGRFAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mboden M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
        188
                                                                                                             128
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                                                                                                  NEPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFI
                                                                                                                                                                                                                                   DARIRPNEKGPPUNUTCNIFINSESSUTKTTMDYRVNVFLRQQWNDPRLSY-REYPDDSL
                                                                                                                                                                                                                                                                                                                                                      GYGLGHCLQARDGGPMEGSGIYSPQPPAPLLREGETTRKLYVD 431
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                                                                                                                                                                                                             DSRIRPNFKGIPVEDKVNIFINSFGSIQETTMDYRVNIFLRQRWNDPRLRLPTDFKSDAL
                                                                                                                                                                                                                                                                                                                LKGLILLMLLVQFSAEEGGKPKKGKKGKQVICPSQLSAEDLDRVPANSTSNILNRLLMTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFGIDTSLSG-DGPLSEAAAMFAGLPPGHALFD---IRRRFVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 AA;
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22 P
56358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
49.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) (Zebra danio);
; Craniata; Vert
Teleostei; Osta
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 876.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
; 12436FC3344F0BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Receptor m
        -SFGYTTKDLVFMWQSGDP-VQMDE-IALPQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4e-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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O1-MAR-2001 (TrEMBLrel. 16
01-MAR-2001 (TrEMBLrel. 16
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF268368; AAG14345.1;
EMBL; AF268339; AAG14345.1;
EMBL; AF268370; AAG14345.1;
EMBL; AF268371; AAG14345.1;
EMBL; AF268372; AAG14345.1;
EMBL; AF268373; AAG14345.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLRB.
                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Ionic Transmembrane. SEQUENCE 497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCĂTION: INTEGRĂL MEMBRÂNE PROTEIN (BY SIMILARITY: -!- SIMILARITY: BELONGS TO-THE LIGAND-GATED IONIC CHANNELS FAMILY. EMBL; AF268376; AAG14347.1; -. EMBL; AF268374; AAG14345.1; -. EMBL; AF268374; AAG14345.1; -. DOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibitory Glycine Receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) TO THE EMBL/GENBANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR00252; NRIONCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pierce K.D., Handford C.A., Healy P.J., Schofield P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09GJS9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bovine Myoclonus is Caused by a Inhibitory Glycine Receptor.";
                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238
                                                     108
                                                                                                                                                                                                                                                                                                                184;
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                                                                                                        63
                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #F268367; AAG14345.1; JOINED.
#F268368; AAG14345.1; JOINED.
#F268376; AAG14345.1; JOINED.
#F268370; AAG14345.1; JOINED.
#F268371; AAG14345.1; JOINED.
#F268372; AAG14345.1; JOINED.
#F268373; AAG14345.1; JOINED.
                                                                                                                                                                                                                                                           9 LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQPM-----
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                             LMGRTSGYDARIRPNFKGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDFR--GSDALTVDPTMYKCLWKPDLFFANEKSANFHDVTQENILLFIFRDGDVLVSMRL
                          -SYREYPDDSLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRL
                                                                                                                                                                                                        VAFFILISL----CIEEAYSKEKSSKKGKGKKKQYLCPSQQSAEDLARVPANSTSNILNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLNSPKRIEAEKIKMAEKEKAREKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DASAARVPLGILSVLSLSSECTSLASELPKVSYVKAIDIWMIACLLYGFASLVEYAVVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAI---
                                                                                                  LL---VSYDPRIRPNFKGIPVDVVVNIFINSFGSIQETTMDYRVNIFLRQKWNDPRLKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Bovine)
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   56039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                      37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16,
                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                        Pred. No. 1.865; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 850.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   82F140C115A887E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.,
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Dennis J.A.,

Pecora; Bovoidea;

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Subunit

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62

107

166

177

Indels Length

Gaps

497; 53;

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RESULT 12
Q9GYU4
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Best Local :
                                                                                                                                              Matches
                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IO EMBL; AY005810; AAF97816.1; -
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; GABAARGAMMA.
PRINTS; PR01620; NEUROTR, ION_CHANNEL; 1.
PROSITE; PS00236; NEUROTR, ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Kirby R.R., Williamson R., Farley S.,

"GABA-A receptor gene sequence from the ce

"GABA-A receptor gene sequence from the ce

cuttlefish, Sepia officinalis.",

cuttlefish, Sepia officinalis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GYU4
Q9GYU4;
01-MAR-2001
                                                                                                                                                                                                                                                                                              Glycoprotein; Ionic channel; Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea;
Sepildae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GABA-A receptor beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                              Transmembrane
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
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           187
                             117
                                               127
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                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-EKIALPQFDIKKEDIEYGNCTKYYKGTGYYTCVEVIFTLRRQVGFYMMGVYAPTLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAEGLTLPQF-ILRDEKDLGCCTKHY-NTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLILSCLMDLKNFPMDIQTCTMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQ
                                                                                     KGPPVNVTCNIFINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDS
                                                                                                      LKYIAMLVLKESTVLIVTLV---LLVGSYGDQSRFQNTTDTIERLL---KGYDIRLRPQF
                                                                                                                 LSFLLLWTLPGQVLLRVALAKEEVKSGTKGSQP--MSPSDFLDKLMGRTSGYDARIRPNF | :: : :::::: || || |::| |
                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLVEYAVVQVMLNNPKRVEAEKARIAKAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AALLEYAAI----NFVSRQHKEFIRLRRRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SITLSCPLDLTLFPMDTQRCKMQLE-----
          TMQLESSSILCSPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDLGC
                                       IWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTC
                                                                  EVQALRIGMEIIIASFDSISEVNMDYTITMYLNQYWTDERLVYSNDSDDNLTLTGDFAEK
                             IWVPDTFFANDKNSFLHDITEKNKMIRLFGNGSIVYGMRFTTTLACMMDLHYYPLDEQNC
                                                                                                                                                                                   486 AA;
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                    56640 MW;
                                                                                                                                                      33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16, Created)
16, Last sequence update)
21, Last annotation update)
                                                                                                                                             69;
                                                                                                                                                     Score 747.5;
Pred. No. 8.86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                    1FD6DBCEC1EC7257 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              from the central
                                                                                                                                              Mismatches
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                                                                                                                                                               DB 5;
                                                                                                                                              109;
                                                                                                                                                                                                                                                                                                                                                                               nervous system
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                                                                                                                                             Indels
                                                                                                                                                                Length
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                                                                                                                                                                                                       Receptor;
                                                                                                                                             23;
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                                                                                                                                             Gaps
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046124;
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                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                        Transmembrane.
                                                                                                                                                                                                                                                                                  Glycoprotein;
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 303
                    236
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horoszok L., Wolstenholme A.D.;
"Ligand gated chloride channel subunits contortus and Ascaris suum orthologues o elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00252; NRIONCHANNEL. TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED
EMBL; Y14234; CAA74623 1; -
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20017520; PubMed=10551358; Jagannathan S., Laughton D.L., Critten C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trichostrongyloidea;
NCBI_TaxID=6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00236; NEUROTR_ION_CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Parasitol.
GLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSRQHKE
                                                         DLGCCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSWVSFWINMDAAPARV
                                                                                                                                        DSIWKPDLFFANEKGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQ
                                                                                                                                                                                                                                                                                   VNIYLRSISKIDDVNMEYSAHFTFREEWVDARLAYGRFEDESTEVPPFVVLATSENADQS
                                                                                                                                                                                                                                                                                                                         CNIFINSESSYTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSML------
                                                                                                                                                                                                                                                                                                                                                                    MLALICTVSTIMSAVEAKRKLKEQEIIQRIL---NNYDWRVRPRGLNASWPDTGGPVLVT
                                                                                                                                                                                                                                                                                                                                                                                                          LLRVALAKEEVKSGTKGSQPMSPSDFLDKLMGRTSGYDARIRPN-----FKGPPVNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEK-LMTPNYQRLSLSFKLQRNIGYFIFQTYLPSILIVMLSWVSFWINHEATSARVALGI
                                    -TKYCTSKTNTGEYSCARVKLLLRREYSYYLIQLYIPCIMLLVVSWVSFWLDKDAVPARV
                                                                                                                                                                                                    QQIWMPDTFFQNEKEARRHLIDKPNVLIRIHKDGSILYSVRLSLVLSCPMSLEFYPLDRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTVLTMTTISNGVRSSLPRISYVKAIDIYLVVCFVFVFAALLEYAAVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVEVE------SYGYTMFDVIMYWRNGKNAVMGVENVELPQFHIKEYKTVVT
                                                                                                                       NCLIDL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 F
50690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemonchidae; Haemonchinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103:129-140(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                       -ASYAYTTQDIKYEWKEQNP-VQQKDGLRQSLPSFELQDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 743.5;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Postsynaptic membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D679BD6BCF67FE1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   115;
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IONIC CHANNELS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 438;
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGRPAMs; TIGR00860; LIC; 1.
TIGRPAMs; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Glycoproteth; Ionic channel; Postsynaptic membrane; Transmembrane.
SEQUENCE 453 AA; 51905 MW; COAD53FA6968CD2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; AJ002232; CAA05260.1;
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E1yBase; EBgn0024963; GluC1-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Semenov E.P., Pak W.L.;
"Diversification of Drosc
posttranscriptional mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUCL-ALPHA OR INDEFINITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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    DLEQ
                                             QRRQ 373
                                                                                                               SGSRASLPKVSYVKAIDIWMAVCLLEVFAALLEYAAINFVSR------QHKEFIRLRRR
                                                                                                                                                                                                   SCLKVDLLFRREESYYLIQIYIPCCMLVIVSWVSFWLDQGAVPARVSLGVTTLLTMATQT
                                                                                                                                                                                                                                                                                                SPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKF
                                                                                                                                                                                                                                                                                                                                                                                  KGANFHEVTTDNKLLRIFKNGNVLYSIRLTLILSCLMDLKNFPMDIQTCTMQLESSSILC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FINSFSSVTKTTMDYRVNVFLRQQWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFFANE
                                                                                      SGINASLPPVSYTKAIDVWTGVCLTFVFGALLEFALVNYASRSGSNKANMHKESMKKKRR
                                                                                                                                                                                                                                                                     -----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                          FVRSISKIDDVTMEYSVQLTFREQWTDERLKFDDIQGRLKYLTLTEANRVWMPDLFFSNE
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21,
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Pred. No. 2.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; DB 5;
2.4e-61;
nes 120;
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Best Local
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STRAIN-OREGON R; TISSUE-HEAD;

MEDLINE-96355334; PubMed-8702744;

Cully D.F., Paress P.S., Liu K.K., Schaeffer J.I

"Identification of a Drosophila melanogaster gluentification of a Drosophila melanogaster gluentification of the antiparasitic agent av.

Channel sensitive to the antiparasitic agent av.

J. Biol. Chem. 271:20187-20191(1996).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO-
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED ION
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01-FEB-1997
01-FEB-1997
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutlamate-gated chloride channel.
GLUCL-ALPHA OR DROSGLUCL OR CG7535.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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TIGREAMS; TIGR00860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U58776; AAC47266.1;
FlyBase; FB900024963; GluCl-alpha.
InterPro; IPR000118; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
SEQUENCE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
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Local Similarity 42.3%;
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                                                                                      352 DLEQ 355
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                                                                                                                                                                                                   SGSRASLPKVSYVKAIDIWMAVCLLFVFAALLEYAAINFVSR------QHKEFIRLRRR
                                                                                                                                                                                                                                                                SCLKVDLLERREFSYYLIQIYIPCCMLVIVSWVSEWLDQGAVPARVSLGVTTLLTMATQT
                                                                                                                                                                            SGINASLPPVSYTKAIDVWTGVCLTFVFGALLEFALVNYASRSGSNKANMHKENMKKKRR
                                                                                                                                                                                                                                                                                                                                                    -----ASYGWTTNDLVFLWKEGDP-VQVVKNLHLPRFTL--EKFLTDYCNSKTNTGEY
                                                                                                                                                                                                                                                                                                                                                                             SPLPSLSLSVGYTMKDLVFEWLEDAPAVQVAEGLTLPQFILRDEKDL-GCCTKHYNTGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                        KEGHEHNIIMPNVYIRIFPNGSVLYSIRISLTLACPMNLKLYPLDRQICSLRM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVRSIMTISDIKMEYSVQLTFREQWTDERLKFDDIQGRLKYLTLTEANRVWMPDLFFSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILYFASLCSASLANNAKVNFREKEKKVLDQILG-AGKYDARIRPSGINGTDGPAIVRINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in; Ionic channel; Postsynaptic membrane; Transmembrane.
456 AA; 52347 MW; 4008E57657566B1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                   373
                      25,
                      2003,
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                      17:16:58
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Pred. No. 3.2e-60;
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Indels Length

Gaps

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456; 29;

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RESULT 13
HSGLYRAL
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Best Local Similarity
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-H.Saplens alpha-2 strychnine binding subunit of inhibitory glycine
                                            450
               123
                                                                                                       943;
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Grenningloh,G., Schnieden,V., Schofiel
Siddique,T., Mohandas,T.K., Becker,C.P
Alpha subunit variants of the human gl
structures, functional expression and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens
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             CATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAACATCTGGATATGATGCCAG
                                            CTTCAGGACGGCTTTCTGCAAAGACCATGACTCCAGGTCTGGAAAACAACCTTCACAGAC
                                                                      CCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGGTCCCAGCC
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LYSIRLTLTLSC PMDLKNEPMDVOTCTIMOLESFGYTMNDLIFEMLSDGPVOVABGLTL
PORILKEEKLGYCTKHYNTGKETCIEVK FHLEROMGYYLIONNI PSLLIVILSWYSF
WINNDARPARVALGITTYLTMTTOSSGGRASLEN YSYYSKAIDIMPAVCLLFVFRALLE
VAAVNEVSROHKEFLRERROKRONKEEDVTRESRENFSGYGMGHCLOVKDGTAVKAT
                                                                                                                                                                                                                                                                                                                           /product="inhibitory glycine
/protein_id="CAA36257.1"
/db_xref="GI:31849"
/db_xref="SWISS-PROT:P23416"
                                                                                                                                                                                                                                                                                                                                                                                      /note="strychnine binding alpha-2 subunit"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="brain"
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1. .1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="fetal"
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                                                                                                                                                                                                                                                            ACTCATCGTCATCCTGGGTCCTGGGTCCTTCTGGATCAACATGGATGCTGCCCCTGCCCG
                                                                                 AGAATTCATACGACTTCGAAGAAGGCAGAGGCGCCAACGCTTGGAGGAAGATATCATCCA 1142
                                                                                                                                                                                  TGTGGGCCTGGGCATCACCACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCCGGGC
                                                                                                                           GGAGTTCCTGCGCCTCCGAAGAAGACACAGAAGAGGCAGAATAAGGAAGAAGACGTTACTCG
       AACAGCTGTCAAGGCCAC
                                   AGGTCCAATGGAAGGTTCTGGCATTTATAGTCCCCAACCTCCAGCCCCCTCTTCTAAGGGA 1262
                                                                  TGAAAGTCGTTTTAATTTTAGCGGTTATGGGATGGGTCACTGCCTCCAAGTGAAAGATGG
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662 964 542

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749 362 689 302 629 242

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| | Dъ | Ay ASSAMASTANAMATUTISANACANGGGTCCCAGCCCATGTCCCCCCTGTATTTCCTAGACA 148 |
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| 1151 GTTTCTATTTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAAGAGATGGAGGTC 1207 | Qy | marches 31/; indets b9; Gaps |
| 1109 AGAGGCGCCAACGCTTGGAGGAAGATATCATCCAAGAAAGTC 1150 | Db Qy | utematable 217, India 60, Cons. |
| ACTITGTGTCTCGGC | ДЪ | BASE COUNT 396 a 508 c 451 g 389 t ORIGIN |
| 1049 ATGCTGCCATAAATTTTGTTTCTCGTCAGCATAAAGAATTCATACGACTTCGAAGAAGGC 1108 | · Qy | |
| 989 AGGCAATCGACATCTGGATGGCTGTGTGTGTCTTGTGTTTGGCTGCCTTGCTGGAGT 1048 | Qy Db | TLILACPMOLKNFPMOVQTCIMQLESSGYMMDLIFEWQEQGAVQVADGLTLPQFILK EEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQWYIPSLLIVILSWISFWIMMDA APARVGLGITTVLTWTTQSSGSRASIDFWAYVCILFVFSALLEYAAVNF VSROHKELLRFRRKRRHHKSPMINIFOEDEAGEGEFWFSAVIMGDATTGAKDGTGVKG |
| 929 TCACCATGACCACAGACCTCTGGCTCCCGGGCCTCTTTGCCTAAGGTGTCCTACGTGA 988 | Ωy | Y LEAD STATE OF THE TOTAL OF TH |
| | Db | /product="glycine receptor alpha 1 subunit" /protein_id="AAG14346.1" /### Prof=" AAG14346.1" |
| 869 CCTTCTGGATCAACATGGATGCTGCCCCTGCCCGTGTGGGCCTGGGCATCACCACCCTGC 928 | Qy | /note="Giralins; alternatively spliced" . /codon_start=1 |
| 809 GCTACTATCTGATTCAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCT 868 | Db Qy | T. 1/44 /gene="Glra1" CDS 229. 1602 /gene="Glra1" |
| 914 ATTACAACACAGGCAAATTCACCTGCATCGAGGCCCGGTTCCACCTGGAGCGACAGATGG 973 | Db | /org |
| 749 ACTACAACACAGGGAAATTCACCTGCATCGAGGTAAAGTTTTCACCTGGAACGGCAGATGG 808 | Qy | |
| 854 GACTAACTCTACCCCAGTTTATCCTGAAAGAGGAGAAGGACTTGAGATACTGCACCAAGC 913 | DЪ | L Submitted Medical R |
| 689 GGCTGACTCTGCCCCAGTTTATCTTGCGGGATGAGAAGGATCTAGGCTGTTGTACCAAGC 748 | . Qy | Healy, P.J. and Schofield, P.R. Direct Submission |
| 797 CCATGAACGACCTCATCTTTGAGTGGCAGGAGCAGGGGGCTGTGCAGGTGGCAGATG 853 | DЪ | |
| 629 CCATGAAAGACCTCGTGTTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGG 688 | Qy | MEDILINE 21109390 PURMED 11178877 |
| 569 TTGAGAGCTCATCCATACTCTGCAGCCCTCTGCCATCTCTGTCACTTTCAGTTGGCTACA 628 | ДУ | TITLE A nonsense mutation in the alphal subunit of the inhibitory glycine receptor associated with bovine myoclonus JOURNAL Mol. Cell. Neurosci. 17 (2), 354-363 (2001) |
| TGGCCTGCCCCATGGACTTGAAGAATTTCCCCCATGGATGTCCAGACGTGCATTATGCAAC | מט | AUTHORS Pierce, K. D., Handford, C. A., Morris, R., Vafa, B., Dennis, J.A., |
| TGTCCTGCCTGATGGACCTCAAGAACTTCCCCATGGACATCCAGACGTGCACGATGCAGC | p oy | Manmalia; Eutheria; Cetartiodactyla; Ruminantia; Pec Bovidae; Bovinae; Bos. 1 (hases 1 to 1744) |
| 659 AACTGCTGAGGATCTCCCGGAACGGGAATGTCCTCTACAGCATTAGGATCACCCTGACAT 718 | DЬ | taurus aryota; Metazoa; |
| 449 AGTTACTGCGCATCTTCAAGAATGGGAATGTGCTGTACAGCATCAGGCTGACCCTCATTT 508 | Qy | S . Bos taurus. |
| 599 CTGACCTGTTCTTTGCCAATGAGAAGGGGGCCCACTTCCATGAGATCACCACAGACAACA 658 | Db | N AF268375 AF268375.1 GI:101 |
| 389 CAGACCTCTTCTTTGCTAATGAGAAAGGGGCCAACTTCCATGAGGTGACCACGGACAACA 448 | Qy | s glycine receptor alpha 1 subunit (Glra1) |
| 539 ATGAATACCCCGATGACTCGCTGGACTTGGACCCCATCCAT | Db | AF268375 AF268375 1744 bp mRNA linear MAM 22-MAY-2001 |
| 329 GAGAATATCCTGGACCTCTGGACCTCGATCCCTCCATGCTGGACTCTATCTGGAAGC 388 | Qy | RESULT 14 |
| 479 TGGACTACAGGGTCAACATCTTCCTGCGGCAGCAGTGGAATGACCCCCGGGCTGGCCTACA 538 | Db | Db 1716 CATTCGCCATGAAGATGTCCACAAG 1740 |
| 269 TGGACTACCGGGTGAATGTCTTCTTGCGGCAACAGTGGAATGACCCACGCCTGTCCTACC 328 | Оу | QY 1383 GCTATGGTCAGAAGATATCCACCAG 1407 |
| 209 CCGTGAACGTGACCTGCAACATCTTCATCAACAGTTTCAGCTCCGTCACCAAGACCACAA 268 | Qу | QY 1323 GGCTGTCTCCCTTTCACTTTCCTCATCTTCAATATCTTCTACTGGGTTGTCTATAAAGT 1382 |
| 149 AACTTATGGGGCGAACATCTGGATATGATGCCAGGATTCGGCCCAATTTTAAAGGCCCAC 208 | D dy | OY 1263 AGGAGAAACCACGCGGAAACTCTACGTGGACCTGAGGCCAAGAGAATTGACACCATCTCCCG 1322 |

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US-10-075-846-4 (1-431) x DRE404970
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Best Local Similarity:
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              GlnLeuGluSerSerSerIleLeuCysSerProLeuProSerLeuSerLeuSerValGly
                                                                                                                                                                                    ATCCTGTCTTGTCCCATGGACTTGAAGAATTTCCCCAATGGACATTCAGACCTGTACCATG
                                                                                                                                                                                                   IleLeuSerCysLeuMetAspLeuLysAsnPheProMetAspIleGlnThrCysThrMet
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TyrThrMetLysAspLeuValPheGluTrpLeuGluAspAlaProAlaValGlnValAla
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GPVLKEEKDLGYCTKHYMTGKFTCIEVKFHLERQMSYVLIQMY 1PSLLTVILSWYSFW
INMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIMMAVCLLIVFAALLEY
AAVNFVSRQHKEFIRLKKQRRQRIEEDLVRESRGFYFRGYGLGHCLQTKOGTAVGGS
SVFAPPPPPVQVLYDGEAVRKRFVDRAKRIDTISRAVFPLSFLIFNVFYWITYKVLRHE
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DFLDKLMGRTSGYDARIRPNFKGPPVNVTCNIFINSFGSITETTMDYRLNVFLRQQWN
DPRLAYSEYPDASLDLDPSMLDSIWKPDLFFANEKGANFHEVTTDNKLLRIFQNGNVL
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/gene="glyR alpha"
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/db_xref="GI:11322384"
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Matches:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1857)
1 (crenningloh,G., Schmieden,V., Schofield,P.R., Seeburg,P.H.,
Siddique,T., Mohandas,T.K., Becker,C.M. and Betz,H...
Alpha subunit variants of the human glycine receptor: primary
structures, functional expression and chromosomal localization
                                                                                                                                                 EMBO J. 9
90183975
                                                                                                                                                                                                                                                                                     glycine receptor;
Homo sapiens.
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EMBO J. 9 (3), 771-776 (1990)
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                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="brain"
/dev_stage="fetal"
388 1746
                       /gene="GLYRA1"
388. .1746
                                                                                                             Location/Qualifiers
1. .1857
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/gene="GLYRA1"
/note="strychnine
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AspLeuGlyCysCysThrLysHisTyrAsnThrGlyLysPheThrCysIleGluValLys
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sdfloklmgrtsgydarirpurkgrpvurtchie insfgsytetymdyrvilelroqw
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Lysirltliscpmdlknfpmdvqtctmglesfgytmndlifemlsdgpvqvaegltl
PQFILKEEKELGYCTKHYNTGKFTCIEVKFHLERQMGYYLIQMYIPSLLIVILSGVSF
WINNDAAPARVALGITTYLTMYTQSSGSRÄSILFKYSYVKAIDIMMAVCLIVFVFAALE
YAAVNFYSROHKEFLRIRROKRQNKEEDVTRESRFNFSGYGMGHCLQVKDGTAVKAT
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/protein_id="CAA36257.1"
/db_xref="GI:31849"
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| CDS | AUTHORS TITLE JOURNAL ATURES SOUICE | REFERENCE AUTHORS TITLE JOURNAL REFERENCE | RESULT 6 RNO310837 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM | Oy 42 Db 159 | Оу 40 Db 154 | Qy 38 Db 148 | Оу 36 Дъ 142 | Qy 34 Db 136 | Оу 32 Db 130 | Оу 30 Db 124 | Qy 28 Db 118 | Qy 26 Db 112 | Db 106 |
|-----|--|--|--|---|---|--|--|--|--|--|--|--|---|
| t t | Groot-Kormelink, P.J. Direct Submission Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Submitted (30-MAR-2001) Groot-Kormelink P.J., Department of Pharmacology, The School of Pharmacy, 29/39, Brunswick Square, London, WCIN 1AX, UNITED KINGDOM Location/Oualifiers 1. 1359 /organism="Rattus norvegicus" /strain="Soraque-Dawley males" | Rodentia; Sciurogr Rodentia; Sciurogr Melink, P. J., Colqul dence of single ch glycine receptors | regicus mRNA for glycine receptor alpha 2 precursor. GI:13548660 ceptor alpha 2 precursor. | 22 GlyGluThrThrArgLysLeuTyrValAsp 431 ::: | ProMetGluGlySerGlyIleTyrSerProGlnProProAlaProLeuLeuArgGlu 421 | 3 SerArgPheTyrPheArgGlyTyrGlyLeuGlyHisCysLeuGlnAlaArgAspGlyGly 402 | 3 PheIleArgLeuArgArgArgGlnArgArgGlnArgLeuGluGluAspIleIleGlnGlu 382 | 3 ValPheAlaAlaLeuLeuGluTyrAlaAlaIleAsnPheValSerArgGlnHisLysGlu 362 | 3 LeuProLysValSerTyrValLysAlaIleAspIleTrpMetAlaValCysLeuLeuPhe 342 | 3 GlyLeuGlyIleThrThrValLeuThrMetThrThrGlnSerSerGlySerArgalaSer 322 | 3 IlevalIleLeuSerTrpvalSerPheTrpIleAsnMetAspAlaAlaProAlaArgVal 302 | 3 PheHisLeuGluargGlnMetGlyTyrTyrLeuIleGlnMetTyrIleProSerLeuLeu 282 | 9 GAACTTGGCTACTGTACAAAGCACTACAACACTGGAAAGTTTACCTGCATTGAGGTCAAG 1128 |

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Query Match
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                                                      protein and polynucleotides are useful for diagnosing and treating disorders related to ataxia. Ataxia gene sequences are useful in gene therapy, and as diagnostic tools or reagents for identifying a characterizing genetic defect involved in the disorders and disease related to ataxia.
                                                                                                                                            Claim
                                   Sequence
                                                                                                                                                                                Novel nucleic acid sequence encoding human ataxia protein for compounds useful for treating disorders relating to mutations
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P-PSDB; AAB19336.
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gamma-aminobutyric acid; OmpF; glycine;

Prepn. of N-terminal extracellular site protein - by culturi E.coli transformed by a plasmid comprising the tac promoter. culturing romoter, ribosome

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The sequence given is the gamma-aminobutyric acid (GABA) A receptor beta-subunit. This sequence is used in an expression plasmid operably linked to the tac promoter, a ribosome binding sequence, the E. coli outer, membrane protein Ompr signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycine receptor alpha-subunit. This expression plasmid can be used to transform E. coli to produce an N-terminal extracellular site protein of ion channel direct binding type receptor.

BP; 171 A; 185 C; 156 G; 145 T; 0 other; Score 366.2; DB 13; Pred. No. 1.6e-94; 0; Mismatches 133; Indels Length 45; Gaps

CCCAGCCCATGTCCCCCTCTGATTTCCTAGACAAACTTATGGGGCGAAACATCTGGATATG CCAAGCCTATGTCACCCTCGGACTTCCTGGATAAGCTTATGGGAAGGACTTCTGGGTATG ATGTGCTGTACAGCATCAGGCTGACCCTCATTTTGTCCTGATGGACTCAAGAACT GGGCCAACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGA TCGATCCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTTGCTAATGAGÂAAG TCAACAGTTTCAGCTCCGTCACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTTGC TCCCCATGGACATCCAGACGTGCACGATGCAGCTTGAGAGCTCATCCATACTCTGCAGCC TTGACCCATCCATGTTGGATTCCATCTGGAAGCCTGACTTGTTCTTTGCCAATGAGAAGG CTCTGCCATCTCTGTCACTTTCAGTTGGCTACACCATGAAAGACCTCGTGTTTGAGTGGC 475 193 133 415 235 73 355 295 535 373 253 475 433

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 Novel nucleic acid sequence encoding human ataxia
                           P-PSDB;
                                                                Rappold-Hoerbrand
                                                                                                                                         23-MAR-2000;
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                                    AspAlaProAlaValGlnValAlaGluGlyLeuThrLeuProGlnPheIleLeuArgAsp
                                                                                     ProSerLeuSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeuGlu
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        The sequence
beta-subunit
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is the gamma-aminobutyric acid (GABA) A receptor sequence is used in an expression plasmid operably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma-aminobutyric acid;
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ABI99254 ABI99254

standard;

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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linked to the tac promoter, a ribosome binding sequence, the E. coli outer membrane protein OmpF signal peptide coding sequence and a sequence coding for the N-terminal extracellular site of either the gamma-aminobutyric acid (GABA) A receptor alpha-subunit or the glycing receptor alpha-subunit. This expression plasmid can be used to transform E. coli to produce an N-terminal extracellular site protein of ion channel direct binding type receptor.
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                                                                                                                                            GACCCATCCATGTTGGATTCCATCTGGAAGCCTGACTTGTTCTTTGCCAATGAGAAGGGG
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                                                                       GluValLysPheHisLeuGluArgGln
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GAAGAGAAGGATCTGAGATACTGCACCAAGCACTACAACACAGGTAAATTCACCTGCATT
                                                                                                                                                                                               LeuProSerLeuSerValGlyTyrThrMetLysAspLeuValPheGluTrpLeu
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                                                              GAGGCCCGATTCCACCTGGAACGGCAG
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